The Journal of HEREDITY

MINIATURE MICE

(See page 95)

Mink Chromosomes

Sex-Linked Late-Feathering Turkeys

Shipper — Wilt-Resistant Watermelons

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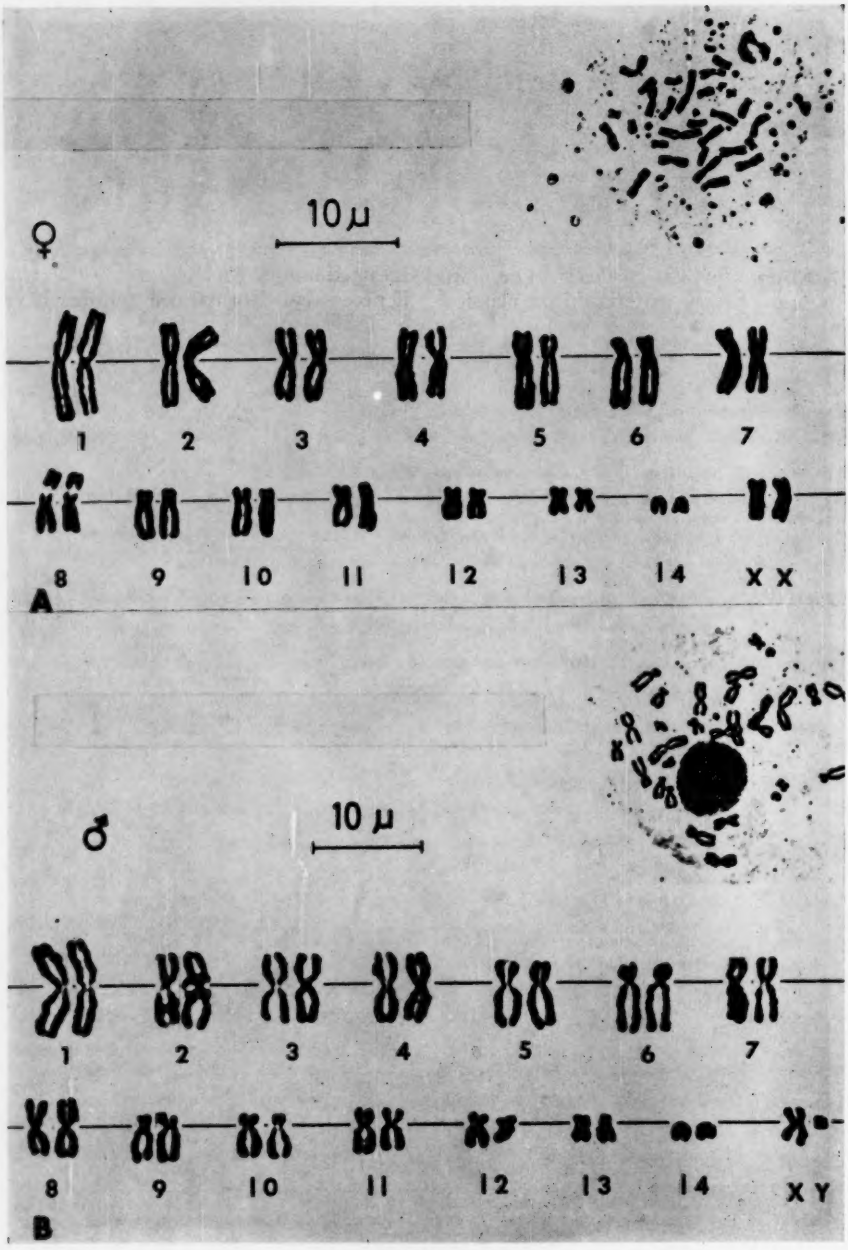


MINK KARYOGRAMS

Figure 1

A—Karyogram of a mink female. The chromosomes of the metaphase cell seen in the upper right corner are arranged according to size and centromere position. The sex chromosomes have been marked XX. No colcemid or colchicine treatment. *B*—Karyogram of a mink male. The chromosomes of the metaphase cell seen in the upper right corner are arranged according to size and centromere position. The sex chromosomes have been marked XY. (Colcemid treatment.)

THE CHROMOSOMES OF THE MINK

KARL FREDGA*

THE chromosomes of the mink (*Mustela vison*, Peale and Beauvois) have been studied by Shackelford and Wipf[5], Lande[4], and recently by Humphrey and Spencer[3]. These authors used testis material in the classical way. The modern tissue culture technique has made it possible to study the chromosomes in different somatic mammalian tissues from both sexes and irrespective of age. In the mitotic metaphases of cells grown *in vitro* we can now study not only the number of chromosomes but also their morphology with greater accuracy than has been possible in the past.

Material and Methods

Thanks to the kindness of Dr. O. Venge, Royal Agricultural College of Sweden, Uppsala, the writer was able, on two different occasions, to take biopsies from minks just killed by electrocution. The animals were of the standard dark color type of ranch-bred mink. On the first occasion, biopsies were taken from the lung and spleen of an adult male (Ad ♂) and from the lung of an adult (pregnant) female (Ad ♀ 1). From this female were taken also two fetuses (F1 and F2), about 7 mm. in length.

On the second occasion lung tissue was taken from an adult (pregnant) female (Ad ♀ 2) and from two fetuses (F3 and F4), 4 cm. in length. The complete fetuses F1 and F2 were minced and cultured, but from the more differentiated fetuses F3 and F4, only pieces of the skin were cultured. It was not possible at this stage to determine the sex of the fetuses, but chromosome analyses later showed that F1, F2 and F3 were females and that F4 was a male.

The technique used is a slight modification of that used as a standard in our laboratories for human skin biopsies[1,2].

Biopsies obtained by sterile removal of pieces of skin, lung or spleen are collected in test tubes containing culture medium to which penicillin has been added. The biopsies may be stored in the medium at +4° C. for several days if necessary. Normal cell cultures have been obtained from biopsies stored for as long as seven weeks.

The specimens are minced with a pair of sharp ophthalmological scissors. This is done in a droplet of medium on a coverslip placed in a Petri dish. Fresh medium is then added (3 ml.). The medium has the following composition:

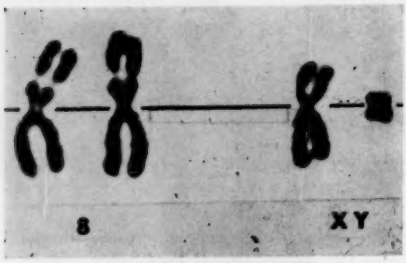
Hanks' balanced salt solution	45%
Pooled human serum	20%
Medium 199 (Difco Laboratory, Detroit)	35%

To each 100 ml. of this medium are added 5 ml. of Bovine Embryo Extract (EE20: Difco Laboratory, Detroit) and 2 ml. of a penicillin-streptomycin solution (100 I.U. penicillin and 1 mg. streptomycin per ml. medium).

The open Petri dish cultures are kept at 37° C. in a common incubator continuously supplied with a suitable amount of CO_2. From the small fragments a monocellular layer grows out over the coverslip. The cultures are regularly inspected with the help of an inverted phase-contrast microscope. The medium should be changed when indicated by the change in color of phenol red, usually every third day (the medium contains phenol red as a pH-indicator). Cells growing on the bottom of the Petri dish may be trypsinized and subcultured, but the majority of these chromosome studies have been performed on primary non-trypsinized cultures. To obtain a sufficient number of mitoses the medium is changed 12 to 18 hours before making the preparation.

For hypotonic treatment the cover-

*Institute for Medical Genetics, University of Uppsala, Sweden. This work was aided by a grant from the Swedish Atomic Research Council to Professor J. A. Böök.



SEX CHROMOSOMES

Figure 2

The satellited chromosomes and the sex chromosomes of the mink. (Colchicine treatment.)

slips with the monocellular layer are transferred to 0.7 percent sodium citrate solution, prewarmed to 37° C. and kept at room temperature.

In some cultures colchicine or colcemid was added to the medium before the hypotonic treatment. The experiments with these prefixation treatments are not yet completed. Various concentrations of colchicine and colcemid have been tried for different lengths of time, the duration of the hypotonic treatment being varied. The data relating to the photographs published in this paper are summarized in Table I.

The cells are then fixed and stained simultaneously in a solution of 2 percent natural orcein (G. T. Gurr) in 50 percent acetic acid for about two minutes. The coverslip is placed inverted on a microscope slide and superfluous fluid removed with filter paper. Squashing is done by manual pressure, controlled under the microscope and repeated until a satisfactory spreading of the chromosomes is obtained. The preparation is then sealed with a mixture of 50 percent collophonium and 50 percent paraffin.

The slides are examined with a ×16 objective and a ×100 oil immersion objective. Concerning the photographic technique, see Table I.

Results

In all, 135 apparently undamaged cells in mitotic metaphase have been analyzed. The great majority of these (117) showed a chromosome number of 30 (see Table II). Deviations from this number are most likely due to technical errors. A few tetraploid cells were observed, and their origin was probably due to endomitosis in the culture. No significant variations in chromosome number and morphology between different individuals or between different tissues were observed.

The chromosome complement consists of seven "large," four "medium" and three "small" autosome pairs. The X chromosome belongs to the medium group and the Y is the very smallest chromosome of the complement.

The morphology of the chromosomes is seen in Figure 1. The chromosomes are here numbered 1 to 14, as nearly as possible according to decreasing length. Usually it is easy to identify the individual chromosomes with the exception of Nos. 2 to 4 and 9 and

TABLE I. Technical data, relating to Figures 1 and 2

Fig. no.	Object	Colchicine or colcemid treatment	Hypotonic treatment	Photo			
				Camera	Original magnification	Film plate	Developer
1*A*	F1 (♀) (complete)	———	10 min.	Zeiss Ultraphot II	1150× (phase contrast, interference filter)	Ilford Chromatic Plate G 30 (9×12 cm.)	Kodak D 11 3 min. (20°C.)
1*B*	F4 (♂) skin	colcemid 0,3 γ/cc medium time: 13 hrs.	5 min.	Zeiss Photomicroscope	400× (phase contrast interference filter)	Adox KB 14 (24×36 mm.)	Adox Microspress 6 min. (22°C.)
2	F4 (♂) skin	colchicine 1,0 γ/cc medium time: 4½ hrs.	3 min.	Zeiss Photomicroscope	400× (phase contrast, interference filter)	Adox KB 14 (24×36 mm.)	Adox Microspress 9 min. (20°C.)

10. Some characteristics of the different chromosomes are summarized in Table III.

Discussion

This investigation confirms the results published previously by Lande[4] and Humphrey and Spencer[3] regarding the number of chromosomes of the mink ($2n = 30$). They identified the smallest chromosome as the Y. The present author has confirmed this and in addition shown that the Y has a median-submedian centromere. Lande as well as Humphrey and Spencer are of the opinion that the X is an acrocentric chromosome. This is not in agreement with the results presented here. In all analyzed cells from males, one chromosome of medium size with a submedian-median centromere lacked a homologue partner. Consequently this one should be the X chromosome.

Neither Lande nor Humphrey and Spencer mention chromosomes with satellites, while Shackelford and Wipf[5] describe two non-homologous satellited chromosomes which they consider to be the sex chromosomes. It is now evident that there are two chromosomes with satellites (No. 8) which, however, are homologous and yet not the sex chromosomes. The secondary constriction is not always distinct in preparations pretreated with colcemid (Figure 1*B*), but otherwise it is seen clearly (Figures 1*A* and 2).

Summary

The number and morphology of the chromosomes in mink have been studied with the cell culture technique. Preparations from cultures of both adult and fetal tissues from both sexes and from different organs have been analyzed. The technique is described. In agreement with Lande[4] and Humphrey and Spencer[3] the chromosome number of the mink was found to be $2n = 30$. The morphology of the chromosomes has been studied, and special attention has been given to the sex chromosomes and to one pair with a secondary constriction (No. 8).

TABLE II. Number of scored cells and their chromosome number from the different cell cultures

Chromosome number	F1(♀) complete	F2(♀) complete	F3(♀) skin	F4(♂) skin	Ad. ♀ 1 lung	Ad. ♀ 2 lung	Ad. ♂ lung	Ad. ♂ spleen	Total
28	—	—	—	1	—	—	—	—	1
30	27	18	11	12	16	10	7	16	117
30±1	2	2	1	—	2	2	1	5	15
32	1	—	—	—	—	—	—	1	2
Cells counted	30	20	12	13	18	12	8	22	135

TABLE III. Some characteristics of the mink chromosomes

Chrom. no.	"Size"	Centromere position	Remarks
1	large	median	The largest one.
2, 3, 4	large	median	These three chromosomes are usually difficult to distinguish from each other.
5	large	submedian	
6	large	subterminal	
7	large	submedian	The smallest of the "large" chromosomes.
8	medium	subterminal	This chromosome has a secondary constriction. The satellites are larger than the short arm. If the satellites were not included in the total length, this chromosome would be the smallest in the medium group.
9, 10	medium	subterminal	These two chromosomes are difficult to distinguish from each other.
11	medium	submedian	Easy to distinguish on the basis of length.
12	small	submedian	
13	small	submedian	
14	small	terminal	The only telocentric chromosome and the smallest among the autosomes.
X	medium	submedian	Sometimes difficult to distinguish from No. 11. The X is yet somewhat smaller and has a more median centromere than No. 11.
Y	small	median-submedian	The incomparably smallest chromosome of all. In preparations not treated with colchicine or colcemid, it is usually impossible to discern the separate arms.

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Research Proposals

THE Division of Biological and Medical Sciences of the National Science Foundation announces that the next closing date for receipt of basic research proposals in the life sciences is September 15, 1961. Proposals received prior to that date will be reviewed at the fall meetings of the Foundation's advisory panels and disposition will be made approximately four months following the closing date. Proposals received after the September 15, 1961, closing date will be reviewed following the spring closing date of January 15, 1962.

Inquiries should be addressed to the Biological and Medical Sciences Division, National Science Foundation, Washington 25, D. C.

MINIATURE, A NEW GENE FOR SMALL SIZE IN THE MOUSE

DOROTHEA BENNETT*

MINIATURE AND NORMAL MICE

Figure 3

Members of the same day-old litter. Normal on left, *mn/mn* on right.

SEVERAL mutations producing small size have been described in the house mouse. One of these, pituitary dwarf[4], has been traced to defects in the anterior pituitary, but for the others, which include methylcholanthrene-induced hereditary dwarfism[6], pygmy[2,3], and diminutive[5], no definite physiological reason for the dwarfing has yet been found. The present paper deals with another similar mutation, designated miniature (*mn*), which behaves as an autosomal recessive lethal with possible partial dominance.

Origin

The mutant *mn* appeared in the descendants of an outcross of Bar Harbor AKR-T mice to the Columbia Brachy stock. The same outcross gave rise shortly afterward to the appearance of another new mutation, *bh*, which has already been described[1]. It is possible therefore that one or both of these mutants was already present but unrecognized in one of the parent stocks, and that the altered genetic background after the outcross permitted greater penetrance or expressivity.

Description

Miniature homozygotes are distinguishable from their normal sibs at birth because of their small size (about three-quarters of normal) and because of a dorso-ventral flattening of the skull (Figure 3). Their initial growth rate is not very different from normal, but very soon they begin to lag behind their normal sibs in this respect, so that with increasing length of life the differential in weight between normal and *mn/mn*

*Department of Zoology, Columbia University, New York 27, N. Y. This investigation was carried out under National Science Foundation Grant 9-6132. The author gratefully acknowledges the assistance of Miss Jo Anne Munigle.

DIFFERENTIATION OF MINIATURE

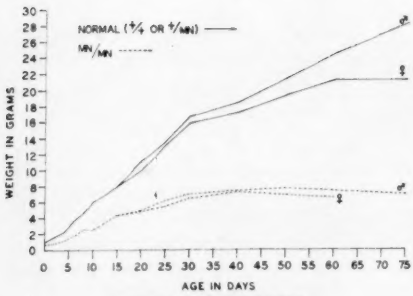
Figure 4

Littermates at six weeks, showing increased difference between normal and *mn/mn*.

becomes greater and greater (Figure 5). Aside from their failure to grow in size and weight, however, *mn/mn* animals do not differ much from their normal sibs; body proportions seem normal, hair and tooth development seem to occur at approximately the normal time, coats are glossy, and behavior is normal (Figure 4). Frequently miniatures are thinner than normal mice, but they do not generally appear cachexic; a sudden severe loss of weight, however, usually shortly precedes death. The mortality for *mn/mn* is heavy at all times, but especially so in the neonatal period. Of a sample of 56 *mn/mn* all of which were alive at birth, 54 percent were dead by the end of the first week, 70 percent by the end of the first month, and 96 percent after two months. A few mutant homozygotes have lived to the age of three or four months; in such cases they were given ample opportunity to mate with normal animals, but all proved infertile. A histological survey of numerous organs and tissues from two sets of like-sex sib pairs of *mn/mn* and normal at birth, 10 days, three weeks, and six weeks did not give any clues to the nature of the defect.

TABLE I. Segregation data

Experiment	Mating type	Offspring (Normal: +/+ or +/*mn*)	*mn/mn*	Total
1	+/*mn* × +/*mn*	513 (79.3%)	134(20.7%)	647
2	+/*mn* × +/+ (outcross)	59	0	59



GROWTH CURVES

Figure 5

Growth curves for normal and *mn/mn* mice, separated by sex. Weights were measured for at least 10 individuals in each category at intervals of two days for the first 10 days, then at intervals of five days for the first month; subsequently an average of five individuals in each group were weighed at weekly intervals.

Genetics

Table I gives segregation data for matings involving animals diagnosed as $+/mn$ by having produced a definite miniature in their first 15 offspring. The table contains only data obtained after the final classification of genotype, and thus the expected frequency of homozygous recessives, assuming full penetrance and expressivity, is 25 percent. The frequency of mutant homozygotes is somewhat lower than expected; this is probably due to the death of some of them before classification rather than to normal overlaps. Thirty-eight animals in the normal group in Experiment 1 (Table I) were progeny tested by the production of at least 15 offspring in matings with known $+/mn$ heterozygotes. Twenty-six of these produced some *mn/mn* offspring and were thus classified as $+/mn$; 12 produced no *mn/mn* offspring and were classified as $+/+$. This ratio of 26 $+/mn$: 12 $+/+$ is in accordance with the 2:1 segregation expected. A group of 11 normal animals from Experiment 2 were tested in the same way, and proved to be 5 $+/mn$: 6 $+/+$; these data are in accordance with the expected ratio of 1:1.

The possibility that *mn* might have effects on size also in the heterozygous condition was investigated. This was done by weighing 20 female sibs of known miniatures at six weeks of age, and then progeny testing them, requiring, as before, a total of 15 offspring from each before classifying the genotype. Fifteen mice completed progeny tests. Their weights and genotypic designation are given in Table II. The over-all genotypic ratio was 9 $+/mn$: 6 $+/+$, not significantly different from the expected 2:1 ratio. It can be seen from the table that if the sample is divided into "low weight" and "high weight" groups, the genotypic ratios are, respectively, 7 $+/mn$: 1 $+/+$ and 2 $+/mn$: 5 $+/+$. Although these ratios are certainly suggestive of a difference in the two classes, neither of them differs significantly, at the 95 percent confidence level, from 2:1. If, however, a chi-square test is done for difference between the "low" and "high" groups, they are found to be significantly different, with chi-square = 8.9, P = 0.02. Thus, *mn* probably has some dominant effect on size.

Comparisons With Other Mutants

No tests have been carried out by matings of miniature with the other mutants producing small size. However, the characteristics of *mn* are clearly not comparable to either pituitary dwarf[4] or diminutive[5]. There are many similarities between pygmy[2,3] and miniature, but pygmy differs by having much greater viability and has body proportions which may not be normal.

TABLE II. A comparison of weights at six weeks and the subsequent genotypic designation of ♀ mice derived from matings of $+/mn \times +/mn$

♀	Weight at 6 weeks in grams	Genotypic designation	
A	14.0	$+/mn$	
B	16.3	$+/mn$	
C	16.5	$+/mn$	
D	16.5	$+/+$	"low group"
E	17.0	$+/mn$	
F	17.0	$+/mn$	
G	17.0	$+/mn$	
H	17.6	$+/mn$	
I	17.8	$+/+$	
J	18.0	$+/+$	
K	18.2	$+/mn$	
L	18.7	$+/+$	"high group"
M	19.0	$+/+$	
N	19.0	$+/+$	
O	19.5	$+/mn$	

Summary

A new autosomal mutant designated miniature (symbol *mn*) has been described in the house mouse. In homozygous condition *mn* reduces size to three-quarters or less of normal, acts as a recessive postnatal lethal, and probably has some effects on size in heterozygotes.

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Genetics in Portuguese

The publication by a Brazilian scientist, Prof. Raul Briquet, Jr., is an excellent exposition in the Portuguese language of basic principles of genetics with special application to animals and man.

It is titled Licoes de Genetica, Part I, and is a publication of Universidade Rural do Rio de Janeiro, 269 pp., 1961. It lacks a bibliography, but this will doubtless be supplied in a later part.

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DOMINANT SEX-LINKED LATE-FEATHERING IN THE TURKEY

V. S. Asmundson and U. K. Abbott*

THERE are numerous reports of variation in the feathering of domestic fowl. These range from the late-feathering of chicks, which when mature have normal plumage[13, 15], to the naked or partly naked, with more than seven genes influencing structure of feathers and over eight genes governing distribution of feathers[1, 6, 10]. Variations in plumage are not confined to chickens; for example, there are porcupine[4] and other mutations in pigeons[11], and penguin guinea fowl[12]. The greater abundance of known mutations is partly a function of numbers of the species, presumably the most important single factor governing mutation frequency; the other factors being the amount and types of breeding programs and of genetic research. In the turkey, hairy was the first inherited feather abnormality reported[14]. A dominant sex-linked late-feathering mutant in the turkey is the subject of this report.

Source and Description of Stock

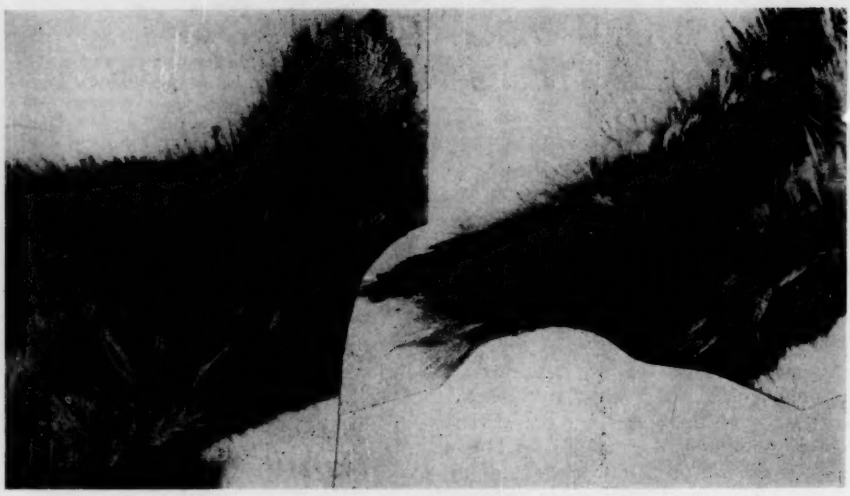
The mutants first appeared in the flock of Mr. G. W. Andrews, Pozo, California, and were reported to one of us by Mr. J. J. MacIlraith, who arranged for breeding tests which clearly indicated that the observed variation in feathering was inherited. Hatching eggs from late-feathering birds were given to the Poultry Department of the University of California, Davis, in the spring of 1954. All the birds that hatched were late-feathering Bronze, medium weight when mature and broad breasted.

Development of down and feathers is delayed. Thus, 16-day late-feathering embryos apparently have shorter down than normal, with some areas between feather tracts virtually free from down (Figure 6). The difference in growth of the flight feathers is readily seen in day-old poults (Figure 7). Normally, five or six primary flight feathers are present on each wing. The late-feathering birds, in the three years—1956, 1957 and 1960—had the following numbers of primary flight feathers: females had none, except in 1960 when the average was 0.86 primaries per wing and 50 percent had wing primaries; males had, on the average, 0.63, 1.41 and 1.97 primaries per wing and the incidence of birds with primaries was 32 percent, 68 percent and 90 percent, respectively. The primaries on the wings of late-feathering birds were relatively short. When eight weeks old, normal birds are usually fully feathered, while late-feathering birds vary from those with few feathers (Figure 8*A*) to those that are relatively well feathered (Figure 8*B*). At maturity the late-feathering birds are still easily identified because of their abnormal tail and wing feathers (Figure 9). Some of the latter resemble juvenile flight feathers, being narrower and more pointed than adult feathers. They also are frequently oriented horizontally on the wing. Missing flight and tail feathers are also common and prevent flight.

LATE- AND EARLY FEATHERING
Figure 6

Sixteen-day-old turkey embryos. Late-feathering left, early feathering right.

*Department of Poultry Husbandry, University of California, Davis.



WING VARIATIONS

Figure 7

Wings of day-old turkey poults. Late-feathering left, early feathering right.

Breeding Tests

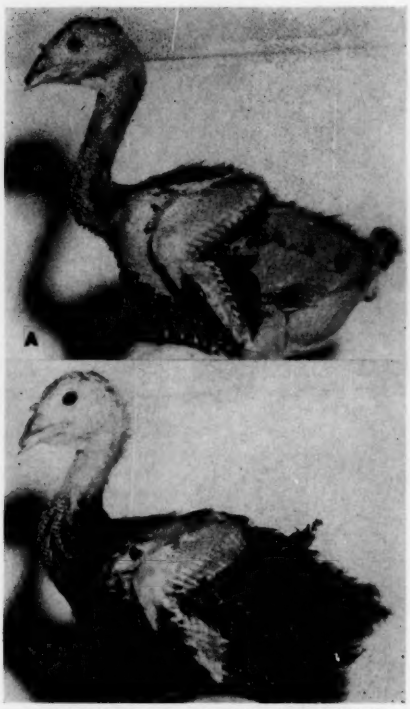
Breeding tests made to determine the mode of inheritance of late-feathering are summarized in Table I. In 1955 one late-feathering male was mated to late-feathering and to normal feathering females. The male was clearly heterozygous as shown by the progeny of the normal dams, while all of the progeny of the late-feathering dams were classified as late-feathering; hence, it seemed probable that the gene for late-feathering was an autosomal dominant. Similar tests in 1956, however, showed that the gene was a sex-linked dominant. Accordingly, a late-feathering Bronze male was mated to Light Brown females in 1957 to obtain heterozygous males to test for linkage between the known sex-linked recessive genes *n* (Narragansett) and *e* (Brown)[2] and the new dominant gene which has been designated *K* because of the apparent similarity of its effect to that of the late-feathering gene in the domestic fowl. The results of further breeding tests made in 1958 to 1960 inclusive (Table I) confirm the results obtained in 1956 and 1957 to show that late-feathering is a sex-linked dominant. Thus, matings of early feathering males × late-feathering females produced late-feathering male and early feathering female progeny. Likewise heterozygous late-feathering males mated to late-feathering females gave only late-feath-

TABLE I. Feathering classifications and sex ratios of progeny, 1955-1960

Year	Phenotypes of parents		Phenotypes of progeny				
			Males		Females		?
	Sire	Dam	Late	Early	Late	Early	?
1955	late*	late	9		8		
1955	late*	early	9	6	4	3	
1956	late	late	6		4		1
1956	late*	late	38		22	14	3
1956	late*	early	20	13	16	16	
1957	early	late	27			27	3
1957	late†	early	16		16		3
1958-60	late*	early	57	38	44	37	
1958	early	late	4			5	
1960	late*	late	19		11	12	

*In each of the three years (1955, 1956, 1960) the same late-feathering sire was mated to late- and normal feathered dams.

†This mating of late-feathering Bronze male to early feathering Light Brown females was made to provide heterozygous males for a linkage test.



DIVERSITY IN LATE-FEATHERING
Figure 8

A—Nearly naked, late-feathering, eight-week-old turkey. *B*—Relatively well-feathered, late-feathering, eight-week-old turkey.

ering male progeny, but both late- and early feathering female progeny were produced in about equal numbers.

Linkage Tests

Linkage between the three mutant sex-linked genes, *K*, *n* and *e*, was measured in the following manner. From late-feathering Bronze males or females mated to early (normal) feathering Light Brown birds heterozygous late-feathering Bronze males were raised. These heterozygous males were mated to early feathering Light Brown and other females. All progeny of the former together with the female progeny of the latter were used to estimate linkage.

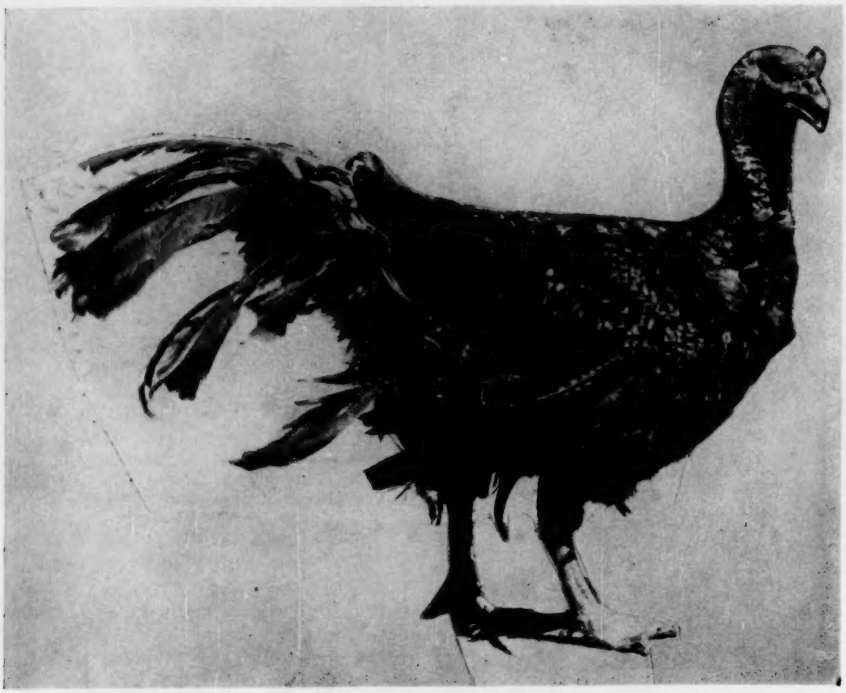
The data in Table II show that the cross-overs in the 167 gametes measured were 25 or 15.0 cross-over units between *K* and *n*, 47 or 28.1 cross-over units between *K* and *e* and 40 or 24.0 cross-over units between *n* and *e*. The indicated order then is *K*-15-*n*-24-*e*. The crossing-over observed in this test between *n* and *e* is lower by about seven cross-over units than previously reported[2]. In view of the variation due to small numbers, the agreement is perhaps as good as could be expected. The main problem in classification was to differentiate, at one day of age or earlier, birds homozygous for *n* from the heterozygotes, i.e., the Narragansett from Bronze, the Light Brown from Brown. By counting only poults, which could be kept if necessary to check the classifications, errors were reduced to a minimum.

Hatchability and Growth

The hatching results are summarized in Table III. An analysis of the data failed to show any statistically significant differences between the early feathering and late-feathering birds in fertility or hatchability. Hence, the data indicate that the late-feathering gene does not affect embryo viability. The high early embryo mortality may have resulted from close inbreeding since the

TABLE II. Linkage tests. All hatched progeny of heterozygous late-feathering Bronze males (*K* + +, + *n e*) mated to Light Brown early feathering females (+ *n e*, ---) are included as well as the female progeny of late-feathering females mated to these same males.

	Males no.	Females no.	Sire gamete genes
Late-feathering Bronze	27	33	*K* + +
Late-feathering Narragansett	1	4	*K n* +
Late-feathering Brown	12	8	*K* + *e*
Late-feathering Light Brown	5	2	*K n e*
Early feathering Bronze	7	2	+ + +
Early feathering Narragansett	7	4	+ *n* +
Early feathering Brown	3	1	+ + *e*
Early feathering Light Brown	21	30	+ *n e*



LATE-FEATHERING MALE

Figure 9

Mature late-feathering male turkey, showing abnormal tail and wing feathers.

matings made varied from those between unrelated birds to brother-sister matings.

The late-feathering gene reduces rate of growth (Table IV). The reduction in size for the first, second and third eight-week periods was calculated[3] from the natural logarithms of the weights in Table IV and an estimated average weight for all day-old birds of 57 grams, and found to be for males 6.2, 8.5 and 3.0 percent and for females 19.5, 17.6 and 3.9 percent. Thus, there was a much greater effect on the percentage rate of growth of females and a slightly greater absolute reduction in the weight of the smaller female. The shanks (tarso metatarsus) and keel of the sternum of late-feathering birds were slightly shorter than those of early feathering birds. Width of breast was not affected.

TABLE III. Summary of hatching results

Feathering phenotype		Set no.	Fertile %	Dead embryos			Hatched	
				Test 1	Test 2	Dead in shell	Crippled	Vigorous
Sire	Dam			Percent of fertile eggs				
Late	Late	314	64.3	18.8	3.5	27.8	1.0	49.0
Late	Early	723	61.1	14.7	0.7	23.1	1.6	60.0
Early	Late	217	73.3	8.2	5.0	17.0	1.9	67.9
Early	Early	656	54.3	25.6	2.0	19.1	2.8	50.6

Discussion

In both the domestic fowl and turkey, early feathering may be regarded as normal or wild-type[8, 9]. In both species the first sex-linked genes identified affected plumage color. It is tempting to postulate that the sex chromosome of both species will be found to have similarly arranged genes. However, it is too soon to claim support for such a point of view because of differences in the plumage color phenotypes in the two species and the paucity of linkage data for the turkey. Even in the domestic fowl, tests of linkage relations of known genes on the sex chromosome[6, 8] are only now being revised and brought near completion[7].

Sex-linked dominant late-feathering in turkeys and chickens are alike in that there is no apparent effect on the down of the day-old bird. The feathers of the wing are delayed in both species with a more easily discernible effect on the turkey. The differences between late- and early feathering birds after hatching are more marked in turkeys. The variation in feathering when eight weeks old is much greater in sex-linked late-feathering turkeys than chickens where feathering of the latter is not complicated by other mutant genes. Mature sex-linked late-feathering chickens are fully feathered and indistinguishable from normal, whereas not all the plumage of adult turkeys is normal, particularly the flight feathers and main tail feathers.

The differences between the species may be due to basic differences in the gene pools of the two species. On the other hand they may reflect the accumulation of genes by domestic fowl which act to modify the effect of the dominant sex-linked late-feathering gene. If so, the original phenotype in the chicken may have been similar to the one now found in the turkey. The late-feathering phenotype of turkeys may become modified by the action of natural or artificial selection to something less extreme. In favor of such an assumption is the marked difference in feathering of eight-week-old sex-linked late-feathering turkeys (Figure 8). Also, the apparent increase in the percentages of such late-feathering birds with primaries in the wings at one day of age, after several generations of outcrossing, argues for modification toward normal feathering through changing the genetic background, or, perhaps more expeditiously, by selection to accumulate favorable genes.

Because of its unfavorable effect on growth this new gene is one that the turkey breeder will want to avoid. Reduction in the weight of late-feathering crossbred domestic fowl was reported by Warren and Payne[16] but was not observed in Rhode Island Reds[5].

Summary

A dominant sex-linked gene in the turkey influences the age at which the first down and first feathers appear. The most obvious effect in day-old birds is on the remiges, the primary flight feathers being absent or reduced below the number usually present and those present being shorter than normal.

Some feathers of later plumages are abnormal, particularly the rectrices and some of the remiges.

The similarities and differences between dominant sex-linked late-feathering in domesticated fowl (*Gallus domesticus*) and turkeys (*Meleagris gallopavo*) are discussed briefly. Because of the similarities to sex-linked late-feathering in domestic fowl the use of *K* is suggested as a symbol for the gene in turkeys.

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TABLE IV. Summary of average body weights and measurements of progeny of segregating families

Feathering phenotype	Sex	Body weight in kilos. 8 wks.	16 wks.	24 wks.	Shank length cm.	Keel length cm.	Width of breast cm.
Early	Male	1.82	5.63	9.18	19.5	17.8	4.19
Late	Male	1.71	4.86	7.68	18.7	16.8	3.94
Early	Female	1.41	4.00	5.80	15.0	14.8	4.07
Late	Female	1.16	2.76	3.85	14.8	13.9	4.12

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Genetic Research

GENETIC RESEARCH. By Arne Müntzing, LTs Förlag, Stockholm, Sweden. 1961. 345 pp. $7.60 approx.

There has long been a need for an excellent elementary genetics text in English which is comprehensive in its treatments of the different facets of genetics yet is written from both the viewpoints of the basic geneticist and breeder. This book, which the author has revised and translated from the text entitled "Arftlighetsforskning" in Swedish, fills that need. Recognition of the excellence of this book outside Sweden has previously been demonstrated by its popularity in the German edition. Professor Arne Müntzing of the Institute of Genetics, Lund, Sweden, is known internationally for his pioneer work in allopolyploidy and also for his practical researches in the utilization of induced polyploidy in rye breeding.

It is a pleasure to review a book dealing with genetics which is organized in a completely logical way and still manages to recognize the historic role of those contributors who have laid the major paving stones along the road of its development. Professor Müntzing has lucidly and simply introduced genetic terms in a functional fashion so that the newcomer to the field is led in easy steps in his understanding. The straightforward style would well form a model for many textbook writers whose native tongue is English.

Although this book has all the desirable elements of an introductory text, sacrifice of the more advanced genetic concepts for the sake of simplicity has not been made. Recent investigations and recently accepted ideas are adequately treated, so even to the worker in genetics it affords a stimulating summary of modern genetic knowledge.

Professor Müntzing's thorough familiarity with genetic researches throughout the world is reflected in this concise and vivid treatment of genetic principles which in this reviewer's experience has not been equaled by other writers. He has made abundant use of excellent diagrams and attractive illustrations, even to demonstrating monozygosis with typically beautiful Swedish girls.

One characteristic which adds greatly to the readability and ease in presentation is the happy neglect of the myriad "workers in the vineyard" during the discussion of the advances made in the science. As much as this contributes to the clarity of the book, this is not always an advantage to the serious student who may be tantalized with a choice tidbit of information without a clue as to where his aroused curiosity might be satisfied. This need has been met to a degree by the inclusion of a complete up-to-date listing of reference books and world periodicals dealing with genetic researches.

Following a short historical introduction, he proceeds from a discussion of the substance of heredity and nuclear division to that of the reduction division in sex cell formation and then to alternation of generations, so that in later chapters explanations of the mechanisms of genetics develop naturally in relation to chromosome behavior. The inclusion of three chapters, not in the original Swedish edition, dealing with the newer researches in physiological and biochemical genetics, the genetics of bacteria, and the nature of the gene extends the scope of treatment so that all the various genetic fields are adequately but necessarily briefly covered. His discussion of mutations both spontaneous and induced is extremely apropos.

The last three chapters touch briefly upon applications in the field of plant and animal breeding and also the relationship of genetics to man himself. A timely warning is given concerning the grave danger that an atomic war would present, quite apart from the immediate destruction of life and civilization—that of "the destruction of the genetic constitution of entire populations."

This book would serve as an excellent elementary text for introducing students from any discipline to the science of genetics.

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PREPARATION AND PARENTERAL ADMINISTRATION OF DNA

From Fowl Erythrocyte Nuclei

R. N. Shoffner, R. E. Burger, C. W. Roberts and A. T. Leighton*

EXPERIMENTAL evidence has demonstrated that genetic information is carried on the chromosomes found in the nuclei of the reproductive cells. Recent biochemical findings indicate that deoxyribonucleic acid (DNA), which is a major constituent of the chromosome, is the molecular template for genetic information. The transforming principle demonstrated in bacteria and obtained in purified form by Avery *et al.*[1] may be reviewed as a type of sexual reproduction in which a genetic element is introduced randomly from an extract rather than as a component of a linear system through the process of fertilization.

A report by Benoit *et al.*[2] dealt with the extraction of DNA from the nucleated blood cells and testes of the Khaki Campbell duck and its injection into the recipient breed Peking. This report suggested the possibility that transformation had taken place. However, the genetic purity of both the recipient and host stocks seems not well established, and segregation and independent assortment may have accounted for the admixture of traits in the progeny. Sirks[5] pointed out that the observed phenotypic changes may not be genotypic. Kushner[3, 4] has reported presumed genetic changes brought about by blood transfusions of one breed of chickens into another. The persistency of these reports does not necessarily minimize their dubious aspects. The short-lived red blood cells and leucocytes transfused to the donor are sources of DNA, and if any transforming principle existed in the cellular elements, its incorporation may explain genetic changes.

It is not known whether the transformation process that seems to occur readily in certain species of bacteria can take place in higher forms. The following preliminary investigations were carried out as a starting point to determine whether transformation could be accomplished in the domestic fowl.

Extraction Procedure

The nuclei from the red blood cells (rbc) of chickens were used as a source of DNA because: 1) large quantities are easily obtained; 2) the same donors can be used repeatedly and later tested for gene frequencies; 3) the DNA found in the rbc chromosomal material is assumed to be biochemically identical to that in the reproductive cells; 4) there is twice as much DNA per rbc as there is in the gametic cell; 5) there are negligible quantities of DNAase or RNA, which leads to a highly polymerized product of reasonable purity and the procedure for isolating DNA is simplified with less chance for loss of activity due to isolation procedure.

Blood (20 to 30 ml. per bird) was drawn by anterior cardiac puncture. Two ml. of isotonic sodium oxalate was used as an anticoagulant for each sample. The blood was filtered through cheesecloth, centrifuged for 20 minutes and washed with cold, isotonic, phosphate-buffered (pH 7.4) saline. The washings were repeated three times, the second and third supernates permitting pulling off the "buffy coat" (white cells) with a suction pipette. Remaining steps were carried out in a cold room (2 to 4°C.).

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The cells were suspended in isotonic buffered saline at one to two times the original volume of blood, and stirred vigorously. One part of 0.3 percent digitonin suspension was added to nine parts of the rbc suspension with stirring, and the cells were permitted to lyse during a period of 15 minutes. The nuclei were packed by centrifugation at 1800 RCF and washed until the supernatant was colorless. The nuclei at this point were straw-colored and the packed volume was generally 60 to 70 percent of the rbc packed volume.

The nuclei were suspended in one to two times the original blood volume of buffered saline with vigorous stirring. An equal volume of sodium chloride solution (10.8 percent w/v) was added quickly to bring the sodium chloride concentration to 1*M* (neglecting volume changes). The nuclei swelled quickly and formed an extremely viscous solution or gel. The solution was vigorously stirred overnight. The resulting viscous solution was shaken with an equal volume of a 4:1 chloroform and isoamyl alcohol mixture. The resulting denatured protein gel was removed by passage through a de Laval separator, the aqueous solution coming out of the "cream" funnel, and the gel and chloroform-amyl alcohol coming out of the "milk" funnel. The aqueous solution was reshaken until resulting gel formation was only minor. The gel-chloroform mixtures from the preceding steps were combined and washed (generally three times) with 1*M* NaCl until only a minor test for deoxyribose was obtained in the aqueous phase. These washings were combined and deproteinization steps previously described were carried out with the 1*M* NaCl supernatant. The resulting gels were combined, washed with a small quantity of 1*M* NaCl and deproteinized.

The 1*M* NaCl solutions were combined and the DNA precipitated by the following steps: a small quantity of the solution was slowly added to 300 ml. of 95 percent alcohol at −5 to −10°C. with stirring. The fibers of DNA wound around the glass stirring rod. The glass rod was removed and the fibers (yellowish to white) compressed to remove the alcohol. The fibers were then removed from the straight glass rod and placed in one-half of the original blood volume of 1*M* NaCl. The alcoholic mother liquor was returned to the freezing room to cool and a fresh, cold solution of alcohol was used for the next precipitation. These steps were repeated until all of the DNA was separated. The resulting concentrated solution of DNA was deproteinized until a gel failed to form by shaking with chloroform-amyl alcohol. The precipitation steps were repeated and the DNA dissolved in sterile, isotonic, buffered saline. The yield by this method was 4,260 mg. DNA from 925 ml. of whole blood. The DNA was dissolved to equal 6 mg. per ml. in all preparations.

The Genetic Material

The DNA was extracted from the nuclei of rbc of donor stocks which carried a number of dominant marker traits easily identified. Pedigree records of both ancestry and progeny allow accurate estimates of gene frequency. These are indicated in Table I. An inbred Rhode Island Red line (Fx = 50 percent) was used as a recipient stock, except for one experiment, since this line is recessive for all dominant markers contained in the donor stock.

Administration and Results

Injections of DNA from donor stock *A* (Run I) were made intraperitoneally at weekly intervals into the recipient chicks. Initial injections in day-old chicks were ½ ml. per week with increasing dosages to 2 ml. per weekly in-

TABLE I. Estimated frequency of dominant marker genes in donor stocks *A* and *B*

		A	*B*
Pea comb	q_P	= .80	= .00
Dominant white	q_I	= .55	= .00
Silver	q_S	= .25	= .45
Barring	q_B	= .20	= .00
Black	q_E	= .25	= .50
White skin	q_W	= .00	= .90
Duplex comb	q_D	= .00	= .15

jection until the chicks reached eight weeks of age.

Run 2 was prepared from *B* donor stock and was injected into recipient chicks in the same manner as Run 1. Table II summarizes this experiment. The control chicks were injected with 0.9 percent saline. In addition, 20 inbred (Fx = 35 percent) White Rock chicks were injected with a total of 60 mg. per chick over an eight-week period. The material was stored at 36°F. during the injection period with no apparent physical change or deterioration during the seven-week storage period. The chicks apparently absorbed the injected material readily without apparent adverse effects.

All chicks were reared in batteries until 12 weeks of age, then transferred to range shelters. When about five months of age, the Rhode Island Red DNA-injected and control saline-injected chicks were sorted into breeding test units. As shown in Table III, 14 injected males were mated by rotation to 29 injected females for a progeny test of possible transformation. An additional eight injected males were mated to recessive non-injected females, making a total of 51 injected individuals test mated. These matings produced a total of 597 progeny. Somatic or genetic changes were not observed in the progeny. None of the DNA-injected chicks (Rhode Island Reds or White Rocks) showed any phenotypic evidence of donor dominant traits.

Injection into Males in Active Spermatogenesis

Two Rhode Island Red males in active spermatogenesis were injected daily with 10 ml. of DNA-I preparation in normal saline for six days followed by 15 ml. daily for 11 days. The site chosen for injection was the subcutaneous space between the inner thigh and abdomen. Untoward effects or evidences of reaction to the material were not found and the solution appeared readily absorbed.

Ten days after the first injection and weekly thereafter for three weeks, pooled semen from these males was inseminated into laying Rhode Island Red hens. While fertility was not particularly high (Table IV), the fertility obtained was approximately characteristic of this inbred line and was probably not depressed due to the DNA injections. All chicks and late embryos examined showed no evidence of dominant traits.

Discussion

Even though no external phenotypic alterations were recognizable in DNA-injected individuals and no changes noted in the offspring of injected birds, the question arises as to the possibility of a *miss* if, in fact, there was a transforming principle present in the extract. In other words—were there enough individuals used as test material to detect a possible transformation?

In order to be detected, absolute specificity of DNA from donor loci to recipient is probably necessary. The injected individuals can be considered as a population of cells, so that if any transformation is accomplished, changes would occur in some cells or part of all cells including the gonadal cells. If the transforming principle is assumed to be based on genetic information in the DNA of the donor chromosomes and its demonstration correlated to gene frequency, an estimate of expected occurrence can be calculated. Assuming a one percent transformation frequency (noted as high as five percent in bacteria) and using the common methods of gene frequency calcu-

TABLE II. DNA injection schedule of recipient chicks

Run or extraction	No. chicks	No. weeks	DNA* Injected/Chick
I	26	8	60 mg.
I	20	8	84 mg.
II	20	8	78 mg.
Control	30	8	0 mg.

*Estimated on basis of 6 mg. DNA per 1 ml. of preparation.

TABLE III. Genetic tests of DNA-injected individuals

Kind of mating	No. ♂	No. ♀	No. progeny
Injected ♂ × injected ♀	14	29	154
Injected ♂ × non-injected ♀	8	24	443
Control ♂ × control ♀	5	12	143

TABLE IV. Fertility of Rhode Island Red males subsequent to injections of DNA preparation

No. ♂	Eggs set	No. fertile	No. hatched
1	100	60	49
1	100	71	59

lation, an estimate of marker trait recoveries can be made.

The somatic check made on the 86 injected chicks showed no evidence of donor phenotype. If one percent or fewer of the cells were altered indiscriminately by donor DNA, the donor characteristics may not be grossly observable. The amounts injected were small compared to the total amount of autogenous DNA present in the recipient.

The breeding tests of injected males × injected females produced 154 chicks, and based on the previous assumptions, about three progeny with one or more of the marker traits might be expected. The mating of injected males × non-injected recessive females producing 443 chicks would produce about four offspring showing one or more of the donor traits. Thus, the probability of detecting the dominant donor traits is undoubtedly of a low order. As the amount of DNA injected is considerably larger than that reported by Benoit[2], the differences in results may be explained by species differences, or by the absence or reduction of transforming activity in the injected DNA.

There are a number of limitations to the successful determination of the occurrence of DNA-mediated transformation in higher forms such as the fowl. Most obvious is that the DNA transforming principle be present in fowl DNA as in certain bacteria. If it is, use of appropriate genetic markers for recognition is essential. The number of markers used in this study seem adequate and in usual genetic tests these traits are definite. The purity of the extracted product may influence the reaction, although crude products show activity in bacteria. Based on biochemical evidence, it is assumed that the DNA of the rbc chromosomes is the same as that of the gametic cells, although this may not be true. The extraction procedure, with the variables of chemical alterations, and with time and temperature effects, most certainly might alter or destroy the principle.

The transfer of donor DNA to recipient sites can be accomplished by various parenteral routes with assimilation into the circulation. Obviously, whether it is metabolized, excreted immediately, or incorporated in some whole or degraded form into nuclear structures would influence the probability of transformation. The age or developmental stage most advantageous for incorporation is unknown, although a logical time would be during or prior to gametogenesis. It hardly seems likely that mature gametes could be altered. A study of factors which could possibly influence detection of transformation is a tremendous task and, of course, a conclusive test is impossible unless a change in phenotype is accomplished. This study by no means precludes the possibility of transformation in the fowl, but under the circumstances of these experiments evidence for its occurrence was not forthcoming.

Summary and Conclusions

A method for preparing a DNA extract from fowl erythrocyte nuclei is described. The preparations secured from dominant donor stocks failed to show any evidence of transforming capability when injected into young, growing, recessive recipient chicks. Adult Rhode Island Red males in active spermatogenesis were injected with DNA extracts and their progeny failed to show any phenotypic change.

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PHYSICAL AND PSYCHOLOGICAL VARIATION AND THE SEX RATIO

MARIANNE E. BERNSTEIN AND MILCIADES MARTINEZ-GUSTIN*

IN a study of alumni of Harvard University, Heath[8] pointed out an interrelationship between physical variation and mental variation and variation in the secondary sex ratio among offspring; i.e., a relationship between body build (Sheldonian somatotype) and sex ratio of children and also between choice of college major and sex distribution of children. Heath suggested that "some common factor may be acting in the body to modify both physique and temperament and sex ratio of the offspring." Since Heath stated that "no definitely corroborative work had been found in the literature," a summary is presented of some of the more important papers on this subject which have been published both before and since the printing of the paper by Heath. Although much work has been done on insects and other lower forms, this report is confined to man and other mammals.

Sex Drive

Rasmussen[12] in Norway investigated genetic differences in the strength of sexual drive in rats, and developed two strains with quite different sex drives. He kept a few records (not enough to allow for a test of statistical significance and reliability) from which this author has computed the sex ratio of offspring. For rats with strong sexual drive the percentage of male offspring was found to be 54.6 percent as against only 48.2 percent for rats with weak sexual drive.

Blood-pH and Sex Ratio

In 1953 Weir[14] selected for variation in blood-pH of mice and found that the strain with high pH showed a high sex ratio at birth, i.e., 56.02 percent males among 598 offspring, whereas the strain with low blood-pH showed a percentage of only 45.58 percent males among 487 offspring. These statistically highly significant differences remained stable through nine generations of inbreeding. Weir postulated a direct physiological relationship between blood-pH and sex ratio; and recently Weir and Wolfe[15] speculated that variations in basal metabolism rates might also be involved. This might lead to an explanation for the somewhat low (41.5 percent ± 7.1 percent) sex ratio this author found in families with one or more children afflicted with Graves' disease[1].

Racial Variation

Extensive data are available on secondary sex ratio variation among different races and subraces of man, the most extensive list having been published by Gini[7]. Korea has been shown to be the country with probably the highest sex ratio in the world[9]. Although much of the national or racial variation in sex ratio may be due to differences in abortion rates, Ciocco[4] believed that the difference between the sex ratio at birth of whites and Negroes in the United States is at least partly due to a genetic difference in the sex ratio at conception. He points out that the secondary sex ratio of Negroes in the United States is about equal to that of Italian immigrants in this country, even though the rate of stillbirths and probably of abortions is considerably lower for Negroes. It is not known, however, whether the sex ratio of the abortions is the same for both groups, nor are there any data available on racial variation of sex ratio among aborted feti.

Occupational Status of Fathers

A statistically significant relationship between occupational status of fathers listed in "Who's Who in America" and

*6 Fair Oaks Terrace, Lexington, Massachusetts, and Bogota, Colombia, respectively.

secondary sex ratio of offspring has been reported in the Italian language[1]. An English translation of the main findings is presented here. In Table I the data which were drawn from the 1948 edition of "Who's Who in America" are summarized. Since length of life is known to have a significant effect on the secondary sex ratio, and in view of the fact that there has been a general upward trend in the secondary sex ratio during the present century, only fathers married between 1910 and 1935 are included. By omitting fathers married after 1935 only "completed families" are included. This is an important limitation not observed in a somewhat similar study by Fancher[6] because (1) Burks[3] found age of reproduction to vary significantly with occupation for men listed in "Who's Who in America," and (2) "incomplete families" contain too great a percentage of first born who are known to have a higher sex ratio than siblings born later.

In view of apparent differences in finding a relationship between occupational status of fathers and sex ratio of offspring in this study as compared to the results obtained by Fancher[6] it is necessary to present a detailed footnote to Table I to show exactly what occupations were included in the 14 larger occupational groups of that table. It will become apparent that Fancher's study included fewer occupational groups, and that several occupations from opposite ends of Table I were grouped together.

During a first attempt to list the sex ratio of offspring for every single occupation (there were more than 50), it became apparent that there was a very close relationship between the sex ratio of offspring for a specific occupation and the percentage of famous women engaged

TABLE I. Incidence of male births, grouped according to paternal profession

Professions	Number of male offspring among 600 children	Percentage of male offspring
Journalists[1]	343	57.17
Physical scientists[2]	337	56.17
M.D. and D.D.S.[3]	336	56.00
Armed Forces[4]	333	55.50
Non-business administrators[5]	333	55.50
Chemists[6]	332	55.33
Engineers[7]	330	55.00
Business administrators[8]	328	54.67
Lawyers[9]	328	54.67
Ecclesiastics[10]	308	50.13
Biologists[11]	300	50.00
Social scientists[12]	279	46.50
Child educators[13]	270	45.00
Artists[14]	270	45.00

[1]Journalists: Editors and writers of *non*-fiction literature, all publishers, news commentators, reporters, political analysts and historians.

[2]Physical scientists: Mathematicians, statisticians, physicists, and astronomers.

[3]M.D. and D.D.S.: Includes only doctors and dentists engaged in actual practice (not in scientific research), excludes psychiatrists and pediatricians.

[4]Armed Forces: Includes all military professions. explorers, gymnasts such as boxers, football coaches, etc.

[5]Non-business administrators: University presidents, deans (except deans of men and women), heads of charitable institutions and hospitals, heads of non-profit research organizations, high school principals and government executives.

[6]Chemists: Chemists, geologists, geographers, agronomists, pharmacists and metallurgists.

[7]Engineers: All engineers and architects except landscape architects.

[8]Business administrators: All professions listed in "Who's Who in Commerce and Industry" (A. N. Marquis Co., Chicago, 1940), and all other economists.

[9]Lawyers: Lawyers, judges and politicians.

[10]Ecclesiastics: Protestant and Jewish clergymen of all ranks, missionaries, instructors at religious colleges, and professors of religion.

[11]Biologists: Botanists, zoologists, physical anthropologists, physicians and dentists engaged in scientific research (except psychiatrists and pediatricians), bacteriologists, and landscape architects.

[12]Social scientists: Sociologists, social workers, philosophers, cultural anthropologists, librarians, professors of languages and literature, psychologists and psychiatrists.

[13]Child educators: Pediatricians, grammar school teachers and principals, and all secondary school teachers (except high school principals).

[14]Artists: Composers, singers, performing musicians (except conductors), painters, sculptors, actors, interior decorators, fiction writers, poets, and art educators.

in that profession and listed in the reference book. Therefore, when it became necessary for statistical purposes to group together related occupations, care was taken to combine only those professions with about equal frequencies of famous women as listed in the reference book. Thus, the large profession of teachers which was left whole by Fancher[6] was broken up into physical scientists, chemists, economists, biologists, social scientists, language teachers, grade school teachers, and teachers of arts and music. Each group of teachers and professors was then combined with men in similar, but non-teaching, professions.

Although most specialists of the medical profession, i.e., surgeons, obstetricians, general practitioners, etc., were men, there were so many women pediatricians and psychiatrists listed in the reference book that these two categories of medical specialists were grouped with child educators and with psychologists, respectively, rather than with practicing physicians. Also, there were somewhat more women physicians engaged in medical research than in actual medical practice, so that research M.D.'s and D.D.S's were listed with biologists in Group 11. Similarly, the large group of writers was broken up, with respect to the percentage of women listed, into a masculine group of non-fiction writers, publishers, news commentators, reporters, etc. (all occupations with very few outstanding women in them) and another group of fiction writers and poets. The latter was combined with all other artists in a group for which many famous women were listed. From the group of business administrators, salesmen were omitted as it was believed that this was not a terminal occupation for many.

We thus have the following differences in classification between the present study and the one by Fancher[6]: the group of educators broken down according to subject matter taught, the group of physicians broken down according to medical specialization, the group of writers broken down into fiction and non-fiction writers, and the group of salesmen entirely omitted. Since the percentage of male offspring differs considerably for the groups after the breakdown (as does the percentage of famous women listed), it seems probable that this suffices (with the possible exception of the occupation of banker) to explain the great difference in results obtained by Fancher and by this writer in the 1951 study. The summary of this study, presented in Table II, shows that the incidence of male births among offspring of men in predominantly male professions (1 through 9) was 8.0 percent $\pm$ 1.3 percent above the incidence of male births for fathers in predominantly feminine professions (10 through 14) and that this difference is statistically highly significant.

Somatotype and Sex Ratio

Choice of occupation is of course a psychological trait which appears to have, as the above relationship between it and the sex ratio of offspring seems to indicate, a physical component. However, since it is only one of several components at best, it would seem more realistic to find a purely physical characteristic in men which might have an effect on the sex ratio of offspring. Such a study was conducted by Martinez[11], who computed the relationship between sex ratio of offspring and physical measurements of parents, the physical measurements being height and weight, combined in the so-called "Rohrer Index." In order to get the strongest possible relationship, the Rohrer index was obtained for both parents and then a new index, M, called "Level of Constitutional Action" by Martinez, was formed by dividing the paternal Rohrer index by the maternal index.

TABLE II. Sex distribution of offspring of fathers in predominantly masculine or feminine professions. (Data from Table I)

Professions of Table I	Total number of offspring	Number of sons	Incidence of male births
1-9	5,400	3,000	55.6
10-14	3,000	1,427	47.6
Total	8,400	4,427	52.6

This was done in view of the fact that Bernstein[2] in a second study had found that the occupations of mothers had a similar effect on sex ratio of offspring as she had found for the occupations of fathers. Martinez applied his index M to two sets of data—one of extreme deviations taken by him, and the one presented by Davenport[5]. As a result of his study, Martinez concluded that the men who had mostly sons, or all sons, are ectomorphs, ectomorphic mesomorphs and mesomorphic ectomorphs. Men who fathered mostly girls, or all girls, are endomorphs, mesomorphic endomorphs, or endomorphic mesomorphs with high endomorphism.

For women, the same author states that endomorphs, endomorphic mesomorphs and mesomorphic endomorphs tend to produce boys. The tendency to produce girls is represented by ectomorphs, mesomorphic ectomorphs, and some ectomorphic mesomorphs having a high degree of ectomorphism. Also, Martinez noted that genandromorphism and ginandrophrenia could be related to the sex ratio, as observed also by Bernstein[1]. However, he did not classify his sample using these "secondary variables."

Summary

A review is presented of research by this author and others pointing to the existence of a genetic mechanism which works to modify the fertilization and gestation processes in such a way that it is not solely left to chance whether an X- or Y-chromosome bearing sperm fertilizes an egg, or whether a male or female zygote is aborted. Furthermore, this research indicates that at the same time this genetic mechanism also has an effect on certain physical and psychological variations of the parent.

In conclusion a possible explanation is given for differing results of this study and one by Fancher on the relationship of occupational status and sex ratio of offspring.

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NATURAL AND RADIATION-INDUCED RECOMBINATION

In *Triticum-Agropyron* Octoploids

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GENERA of the Triticinae provide a number of examples of polyploid series with a base number of $x = 7$ chromosomes. Sources in this group are now available from which new wheat-like species may be synthesized at the octoploid level. Presumably such species might (1) permit the stabilization of possibly higher types of resistance to diseases, and (2) combine unique quality and agronomic characteristics.

Hybridization of decaploid *Agropyron elongatum* and common wheat followed by selection in segregating generations has led to fairly stable octoploid types with high levels of disease resistance. However, kernel type, test weight, threshability, and other characteristics of these types are generally unsatisfactory. Furthermore, without induced recombination, selection within hybrids of these octoploids and hexaploid wheats has failed to yield acceptable recombinations of desired characteristics.

A number of octoploid forms derived mainly from the doubling of tetraploid *Triticum* species hybrids cross fairly readily with the *Agropyron elongatum-Triticum vulgare* octoploids. An opportunity was presented, therefore, to test the effectiveness with which X-radiation and thermal neutrons might induce translocations between chromatin of various parental octoploids. Comparisons of the multivalent chromosome associations at meiosis in control and irradiated M_1† populations, correlated with the appearance of octoploid or near-octoploid types which present recombinations of characteristics in M_2, were considered as a measure of the degree of effective genetic rearrangement achieved. Since these are chiefly self-fertilizing forms, structural heterozygosity is quickly reduced to homozygosity; therefore, selection for fertility plus further hybridization, irradiation and selection can be applied.

Materials and Methods

The crosses among various octoploids were made in the wheat nursery at the Washington Agricultural Experiment Station, Pullman, Washington, during the 1956 growing season. *Agropyron*-wheat octoploids SH 191 and SH 198 were used as pollen parents. These octoploids were used by Larter and Elliott[3], Osborne and Elliott[5], and Elliott[1]. Seed of the octoploid wheats was generously supplied by Dr. B. C. Jenkins, Division of Plant Science, University of Manitoba, Winnipeg, Manitoba. The sources of these materials have been outlined by Elliott[2].

A dose of 14,000 r of 34 Kvp X-rays was applied to the dormant F_1 seed at Washington State University just prior

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†M_1 = first generation following mutagen (or control) treatment.

to planting. Additional F_1 seeds of five combinations were subjected to a flux of approximately 1.3×10^{13} n^{th}/cm^2 through the generous cooperation of the Brookhaven National Laboratory, Upton, New York.

Agronomic characteristics recorded included emergence, habit of growth and mature height of M_1 plants.

Cytological analyses were conducted on M_1 and M_2 plants of control and irradiated populations. Spikes were fixed, stored, and smeared according to the technique described by Newcomer[4]. The occurrence of the following chromosome relationships was recorded: univalents; open, closed, and heteromorphic bivalents; multivalents; and interchanges.

Correlation of *2n* number with various chromosomal configurations and fertility was studied in the M_2 generation. Segregation of agronomic characteristics of M_2 progenies from the fertile hybrids was recorded for plants grown during the 1958 season. The following plant characteristics were considered: (1) spring or winter growth habit; (2) grass-like forms and their number; (3) parental types (like SH 191 and SH 198); (4) wheat-like plants, classified according to culm thickness and color, leaf shape and size, spike shape and length, and threshability; (5) fertility; and (6) kernel shape and size.

Results

The M_1 generation

Emergence, survival and fertility of control, and the M_1 irradiated plants of certain X-ray and thermal neutron treated populations are presented in Table I.

The percent emergence and survival of M_1 plants for all crosses was lower in the X-ray treatment than in the thermal neutron treatment, confirming data of Osborne and Elliott[5] and Larter and Elliott[3]. Five of seven combinations planted produced partially fertile M_1 plants. The hybrids of (*A. tricophorum* × *T. durum*)^2 with both SH 191 and SH 198 were the most fertile of combinations studied irrespective of radiation treatment. Hybrids involving (*T. timopheevi* × *T. orientale*)^2 × SH 191 and SH 198 grew vigorously, and produced a large number of culms with well-developed spikes, but were completely sterile.

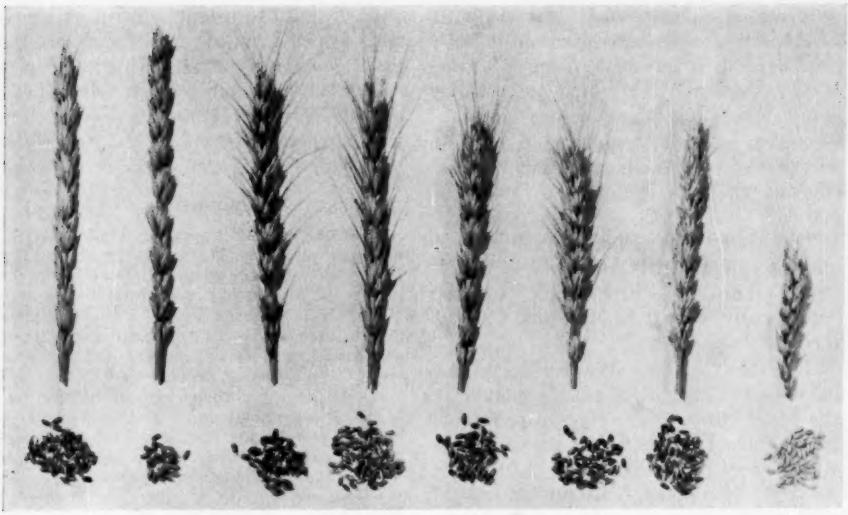
Both control and irradiated M_1 plants of all crosses were quite grass-like in their leaf characteristics, culm thickness, height, and general appearance; the nodes were thick, purple colored, and the spikes long. Seeds produced on the semi-fertile hybrids were long, tapered, and grass-like. They ranged in color from red, light blue, to green, indicating segregation for endosperm color.

Meiotic analyses of 64 plants represented by 1054 pollen-mother-cells of the M_1 populations are presented in Table II.

Meiotic analyses revealed fairly regular chromosome behavior in some hybrids while irregularities, such as fragments, univalents, heteromorphic bivalents, and isochromosomes were found in others. Multivalent associations were present in the meioses of the partially fertile hybrids in both the control and irradiated M_1 populations. Associations of five, six, and occasionally eight chromosomes occurred in both combinations in-

TABLE I. Emergence, survival, and fertility (seed set) percentages for irradiated *Triticum-Agropyron* M_1 populations

	Treatment	Emergence	Survival	Fertility
	control	62	74	25
	X-ray	29	60	18
(*A. tricophorum* × *T. durum*)^2 × SH 198	N^{th}	70	87	24
	control	75	89	25
	X-ray	33	67	19
(*A. tricophorum* × *T. durum*)^2 × SH 191	N^{th}	72	78	21
	control	42	60	10
	X-ray	30	33	8
(*T. timopheevi* × *T. polonicum*)^2 × SH 198	N^{th}	78	88	6



SPIKE AND KERNEL TYPES

Figure 10

Array of M_2 spike and kernel types from the cross (*A. tricophorum* × *T. durum*)^2 × SH 198.

volving (*A. tricophorum* × *T. durum* var. Pentad)^2. Multivalents appeared to be most frequent in plants from neutron-treated seeds and were more frequent in plants from the X-ray treatment than from the control. The increase in multivalents observed in the M_1 over those observed in the control may be explained most satisfactorily as induced translocations. In this regard neutron treatment was most efficient, particularly for the (*T. timopheevi* × *T. polonicum*)^2 × SH 198 cross.

The M_2 populations

In contrast to the M_1, the M_2 populations displayed variation for such morphological characteristics as winter versus spring growth habit, culm color, height, spike type and density, awns, and various kernel characteristics (see Figure 10).

The highest number of wheat-like plants of all spring types studied at the octoploid level (55-56) was found in the neutron treatment, whereas none was found in the controls (see Table III).

TABLE II. Mean chromosome association per pollen-mother-cell in M_1 plants examined

		Chromosome association				
	Treatment	I	II	III	IV	V-XII
(*A. tricophorum* × *T. durum*)^2 × SH 191	control	3.1	25.7	.09	.16	.03
	X-ray	3.8	25.1	.13	.63	.07
	N^{th}	2.7	24.4	.19	.63	.12
(*A. tricophorum* × *T. durum*)^2 × SH 198	control	4.6	24.1	.26	.38	.03
	X-ray	7.6	22.2	.36	.46	.09
	N^{th}	4.3	23.6	.40	.53	.10
(*T. timopheevi* × *T. polonicum*)^2 × SH 198	control	11.3	21.5	.38	.21	—
	X-ray	13.3	20.2	.18	.22	—
	N^{th}	11.4	19.0	.55	.47	—

Wheat-like octoploid plants with wheat-like kernels were observed in both combinations involving (*A. tricophorum* × *T. durum*)^2. Of those wheat-like plants which were analyzed cytologically, a majority were found in the neutron treatments. A maximum number of 52 chromosomes was found in M^2 control plants.

The M_2 irradiated plants examined at meiosis ranged from $2n = 44$ to $2n = 58$ for all crosses. Chromosome numbers occasionally varied in different cells of the same spike.

The meiotic chromosome associations in pollen-mother-cells of M_2 plants in the 54-56 chromosome class are presented in Table IV. Multivalent associations were higher in the irradiated than in the control populations, an indication of structural heterozygosity remaining from induced interchanges. Again, as in the M_1, plants from the radiation treatments had the highest number of multivalents, indicating that the frequency of translocations was also greater.

Using the increase in number of multivalents in irradiated M_1 and M_2 meioses over those of the control as a criterion of induced translocation, the thermal neutron treatment applied was somewhat more efficient in this experiment. Neutron treatment was even more useful when the survival of plants from the treated seeds was considered.

Summary

Cytogenetic studies were conducted on the first and second generations of irradiated and non-irradiated seeds from *Triticum-Agropyron* crosses. The percent survival of M_1 plants of all crosses was lower in the X-ray treatment than in the thermal neutron treatment. Among the hybrid combinations studied, (*A. tricophorum* × *T. durum*)^2 crossed to both SH 191 and SH 198 produced plants of highest fertility. Meiotic analyses of irradiated and control M_1 populations revealed the highest frequency of multivalents in the neutron treatments. Among the spring-type segregates, at the octoploid level in M_2, the greatest number of wheat-like plants was found in the neutron treatment. Control plants with a maximum of only $2n = 52$ chromosomes were found. Meiotic analyses of M_2 plants revealed that those in the neutron treatment carried the highest number of multivalents. Using the increase in number of multivalents in irradiated M_1 and M_2 meioses over those of the control as a criterion of induced translocation and survival of plants from irradiated seeds, the thermal neu-

TABLE III. Observed frequency of wheat-like M_2 plants with wheat-like kernels according to chromosome classes from PMC analyses

	Treatment	No. of plants	Number wheat-like	Chromosome classes 55-56 or more	52-54.9	49-51.9	46-48.9
	C	100	20	..	1	1	..
(*A. tricophorum*	X	98	28	2	2	2	3
× *T. durum*)^2 × SH 198	N	166	52	7	2	..	..
	C	96	13	..	..	1	1
(*A. tricophorum*	X	63	9	1	1	..	..
× *T. durum*)^2 × SH 191	N	104	32	2	1	..	..

TABLE IV. Mean meiotic chromosome associations in pollen-mother-cells of M_2 plants in the 54-56 chromosome class (total of 693 PMC's in 55 plants)

		Chromosome association I	II	III	IV	V-XII
(*A. tricophorum* × *T. durum*)^2 × SH 191	control	4.5	24.4	.26	.41	.05
(*A. tricophorum* × *T. durum*)^2 × SH 198	control	4.4	24.5	.36	.33	....
(*A. tricophorum* × *T. durum*)^2 × SH 191	X-ray	4.7	23.4	.37	.58	.15
(*A. tricophorum* × *T. durum*)^2 × SH 198	X-ray	3.8	23.5	.54	.52	.08
(*A. tricophorum* × *T. durum*)^2 × SH 191	neutron	3.4	23.2	.44	.67	.26
(*A. tricophorum* × *T. durum*)^2 × SH 198	neutron	3.8	23.9	.45	.52	.07

tron treatment was the more efficient in this experiment.

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MAMMALIAN GENETICS AND REPRODUCTION

THIS symposium* is the thirteenth in a series sponsored by the Biology Division of the Oak Ridge National Laboratory in cooperation with the Division of Biology and Medicine of the Atomic Energy Commission. It consists of 12 papers given at a research conference held in Gatlinburg, Tennessee, April 4-7, 1960, and dedicated to Sewall Wright, "in honor of his penetrating experimental and theoretical contributions and with appreciation for his inspiring combination of mathematical elegance and intuition for biological realities."

The intent of the conference, as noted by Alexander Hollaender in a brief introduction, was to bring together geneticists to review and assess recent findings and to suggest lines of research for future development. The program was an ambitious one, covering all fields of genetics and many phases of reproductive physiology. Its comprehensive nature is indicated by the table of contents: Anomalies of fertilization leading to triploidy by C. R. Austin; Genetic influences on the morphology and function of the gametes by A. W. H. Braden; Embryological phases of mammalian gametogenesis by Beatrice Mintz; Developmental genetics in the mouse, 1960, by Hans Grüneberg; Genetics in relation to reproductive physiology in mammals by W. F. Hollander; Current status of mammalian immunogenetics by Ray D. Owen; The inheritance of hemoglobin types and other biochemical traits in mammals by Salome Gluecksohn-Waelsch; Phenogenetic aspects of some hair and pigment mutants by Herman B. Chase and Stanley J. Mann; Mammalian pachytene chromosome mapping and somatic chromosome identification by A. B. Griffen; The genetics of vital characters of the guinea pig by Sewall Wright; The genetics of litter size in mice by D. S. Falconer; and Genetic analysis of induced deletions and of spontaneous nondisjunction involving chromosome 2 of the mouse by Liane Brauch Russell and W. L. Russell.

Many of the papers contain figures and all cite numerous references from the literature. Each formal paper is followed by an "open discussion," reprinted in the symposium volume. Many of the comments, questions and answers in the discussions undoubtedly are valuable contributions to the subject matters under review; in general, they will serve to remind the reader that even "basic findings" are subject to interpretation depending on individual experience.

The mammal most often referred to is the laboratory mouse. Only one paper, that of Sewall Wright, deals exclusively with another mammal, the guinea pig. This monumental review covers many years of study and observations on a colony of over 120,000 guinea pigs of different inbred strains. As a result of many analyses, Dr. Wright concludes that the occurrence of unfavorable morphological abnormalities, many of which were studied in detail, has no great significance in the vital statistics of the colony. The important role is that of genetic differences in such vital characters as frequency and size of litters, percentages born alive and reared, birth weights and early gains. The other paper in the field of population genetics is concerned

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with the complex question of the effects of inbreeding and selection on litter size. The mouse is the mammal used and the quantitative character chosen is the number of young born alive in first litters. About 40 percent of the reduction in litter size with inbreeding is attributable to reduced female fertility (increased preimplantation loss of eggs and embryos), the remaining 60 percent to reduced viability of young. An interesting finding is that ovulation rate is not reduced.

The paper on immunogenetics covers researches on a variety of mammals including man in areas of current greatest interest. Subjects emphasized are: genetic control of cellular and soluble antigens; tissue transplant incompatibility; reproduction and maternal-fetal interaction; and the genetics of antibody formation. In cytogenetics, the preparation and uses of a simplified pachytene chromosome map of the mouse are described. Other papers, none of which will be reviewed in detail, cover the fields of formal, developmental and physiological genetics, the genetics of gametes, and genetics in relation to several phases of reproductive physiology.

The reader can not help but be impressed by the important role played by the inbred mouse and its many mutant forms in supplying investigators with keys to the solutions of basic problems. In paper after paper, tribute is paid to one or more mutants, spontaneous and induced, without which important phases of the investigations would have been difficult if not impossible. The accumulation of large numbers of independent mutations provided tools for a detailed genetic analysis of a specific chromosome region, the *dilute-short-ear* locus. This analysis involved producing over 50 kinds of homozygotes and making over 100 combinations of independent mutations and deletions. Translocations were the basis for the identification of 10 of the possible 20 linkage groups on the pachytene chromosome map.

Interstrain variations in the form and function of gametes indicates that genetic constitution affects the development and function of gametes in animals, as has long been known to be true in plants. Unequivocal evidence of a genetic influence on gamete function comes from studies of the multiallelic *T* locus. Gene action at this locus is postreductional, affecting sperm transmission, and resulting in selective fertilization and a marked departure from the "rule" of random union of gametes. Several of the *d se* mutants, produced by irradiation of postspermatogonial stages, also are transmitted with less than normal frequency, possibly because of semilethal effects on gametes. Such findings of gene effects on the survival and function of gametes have initiated a new branch of genetics, gametic genetics, concerned with expression of factors prior to fertilization.

Studies of mutants at the *W* and *Sl* loci nave supplied evidence against the long held concept of postnatal neoformation of germ cells from somatic cells. In mice homozygous for these genes, a pronounced deficiency of primordial germ cells in embryonic life leads to a sterile gonad in the adult male and female. This fact and other evidence from irradiation of gonads and isotope labelling indicates that germ cells develop early in embryonic life and that mitotic descendants of the same cell lineage persist to maturity in the adult. These same genes, with others, have provided the tools needed in studies of the relation of genes to such products as hemoglobins, pigments, antigens and enzymes. The hair and pigment mutants facilitate the study of the chains of biochemical processes which take place between gene and definitive phenotype because it is possible to observe developmental and physiological processes in fetal, postnatal immature, and adult mice.

Embryological data on 42 mutants are summarized in tabular form and the conclusion made that methods other than morphological will be necessary before primary gene action can be determined. Studies of development, while giving knowledge of the points at which abnormal processes are expressed morphologically, have contributed little to recognition of points where the essential processes break down. In only a few mutations, such as albinism, is the point of biochemical defect detectable visibly. Serological techniques are suggested as the most likely to succeed.

Because of the difficulties involved in making and interpreting interspecies crosses, genetic bases of differences in reproductive physiology can not be analyzed easily. Studies of defective types, such as those with male sterility, and others with incompatibility between mother and fetus offer a means of gaining insight into genetic influences on different phases of reproductive physiology. Among abnormalities that occur during fertilization, triploidy is the commonest. This chromosomal aberration may come about in several ways, one of which arises from polyspermy. Observations on strains of mice and rats show that the mammalian egg has lines of defense against polyspermy, that the efficiency of the defense mechanisms varies with genetic constitution and can be influenced by experimental means. The genotype of the female is thus shown to be an important factor in determining the incidence of triploidy.

The authors who surveyed these broad, complex fields so efficiently manage to convey to the reader not only the many exciting discoveries of recent years, but also some of the problems remaining to be solved and indications of what the future may bring. Any biologist, whatever his area of special interest, should enjoy and profit from reading this volume.

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BREED DIFFERENCES IN STORING CHICKEN SEMEN

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A METHOD has recently been devised at this laboratory whereby chicken semen can be stored for periods up to two days with only a moderate reduction of fertilizing ability[3]. Since this research was done using males of a Flightless breed and White Leghorn females, an experiment was designed to determine if semen from other breeds could be stored equally well. There have been no previous reports on differences among strains or breeds of chickens in the fertility of their stored semen.

Experimental Procedure

Three trials were conducted involving males of three breeds: White Leghorn, Red Vantress, and a Flightless breed which originated mostly from the New Hampshire breed. Semen was inseminated in all cases into White Leghorn females. The males were trained before the experiment and were used for collection two days before semen was collected for fertility studies or sperm count. The method of semen collection was a one-man technique previously described[1]. Since the quantity of semen collected from each male was rather small, all of the semen collected from the males on a given day was stored. Two days later this semen was inseminated into the females, and on the same day a second sample of semen was collected from these males and inseminated within an hour after collection. The exception to this was Trial 2 in which the semen to be inseminated fresh was collected and inseminated first and two days later semen for storage was collected and inseminated after a storage period of approximately two days.

The procedure for storing semen was to dilute it 1 to 10 (*i.e.*, one volume semen and nine volumes diluent) immediately after collection with a sodium phosphate buffer containing 4 mg. fructose, 200 mcg. oxytetracycline and 1000 mcg. dihydrostreptomycin per ml., and 10 percent egg white. It was then stored at 10°C. in graduated centrifuge tubes with cotton plugs. Just before insemination, the diluted semen was centrifuged at 1200 R.C.F. for 10 minutes, the supernatant discarded, and the sample brought to its original volume by resuspending the sperm in buffer containing 4 mg./ml. fructose.

The order in which semen samples and hens were used in insemination was randomized. One-tenth ml. semen was inseminated using an extension tube similar to that used by Parker *et al.*[2] Hens with a hard-shelled egg in their oviduct were not inseminated. Two eggs were saved from each hen before insemination to confirm that the hen was infertile. Eggs laid on the second through fifteenth day after insemination were candled after five days of incubation; any questionable eggs were broken out and observed macroscopically for embryonic development. Hatchability was computed as the number of fertile eggs that had hatched by the twenty-second day of incubation.

In each trial an average of four males per breed and four hens per male were used. The fertility data for each breed and trial are based on an average of 76 eggs per figure (Table II). Statistical significance of the differences was determined by chi-square. The actual storage time for the semen ranged between 48 and 50 hours. The sperm count was determined on a separate collection of semen from the same males used in the

*Department of Poultry Husbandry, University of Maryland, College Park. Scientific Article No. A870. Contribution No. 3180 of the Maryland Agricultural Experiment Station, Department of Poultry Husbandry. The authors are indebted to Richard Seagrave for technical assistance.

fertility trials.

Results

There was no apparent difference among the three breeds in their sperm count (Table I). Fertility and hatchability data are given in Table II. When fresh semen from different breeds was used, no significant differences in fertility resulted; the only exception was in Trial 1, in which second-week fertility from semen of the White Leghorns was significantly higher ($P = <.05$) than that of the other two breeds. Results with the stored semen, however, showed that in each trial the fertility during the first week after insemination was significantly higher ($P = <.005$) when the semen was from the Flightless breed rather than from the other two breeds; in the case of the second week after insemination, the differences among the breeds were only significant in Trial 2 ($P = <.005$). No significant differences among breeds were observed in the hatchability of fertile eggs. Apparently some of the difference among breeds in fertility from stored semen can be explained by a different percentage of hens that laid at least one fertile egg; this percentage was significantly higher for the Flightless breed in Trial 1 ($P = <.05$) and Trial 2 ($P = <.10$) than for the White Leghorn.

TABLE I. Sperm count of males used in fertility experiments

Trial no.	Flightless	White Leghorn	Red Vantress
	Millions per cu. mm.		
1	3.9	3.2	3.4
2	4.0	4.5	—
3	3.2	3.9	—
Ave.	3.7	3.9	—

Discussion

These results provide an instance of marked differences among breeds of chickens in the *in vitro* storing ability of their semen, even though they do not differ in their *in vivo* storing ability as measured by the fertility from fresh semen. These data do not reveal whether these are differences due to breed or strain, since each breed was represented by only one strain. It is somewhat distressing to observe

TABLE. II. Fertility and hatchability from fresh and stored semen collected from different breeds of chickens when inseminated into White Leghorn hens

	Fresh semen			Stored semen		
Trial no.	Flightless	White Leghorn	Red Vantress	Flightless	White Leghorn	Red Vantress
	Percent of hens that laid at least 1 fertile egg					
1	100	100	81	86	40	63
2	100	100	—	88	53	—
3	79	89	—	67	41	—
Ave.	93	96	—	80	45	—
	Percent fertility 1st week after insemination					
1	92	92	84	56	16	23
2	93	91	—	76	30	—
3	70	82	—	42	17	—
Ave.	85	88	—	58	21	—
	Percent fertility 2nd week after insemination					
1	36	68	48	4	0	6
2	54	53	—	23	5	—
3	45	57	—	3	1	—
Ave.	45	59	—	10	2	—
	Percent hatchability of fertile eggs					
1	98	87	93	97	100	96
2	83	88	—	96	96	—
3	85	91	—	78	100	—
Ave.	89	89	—	90	99	—

that methods for storing semen *in vitro* that have been developed with one breed cannot necessarily be applied with equal success to a second breed. It is possible that the research done with the Flightless males has established optimum conditions for storing the semen of this particular breed, but that different conditions are optimum for the semen of White Leghorns. In this case the difference among the breeds would be a difference in the optimum conditions for semen storage rather than in the ability of their sperm to withstand storage. It should be noted that this study has dealt with only one aspect of breed differences in the fertility from stored semen. Other differences may also exist due to the breed of hen.

Summary

Semen from three breeds of chickens (White Leghorn, Flightless, and Red Vantress) was stored for two days prior to insemination into White Leghorn hens. The stored semen from the Flightless breed produced significantly higher fertility than did that from the other two breeds. No breed differences were found in fertility from fresh semen, hatchability of eggs fertilized by fresh or stored semen, or in sperm count.

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GENETICS OF THE CLAYBANK DUN HORSE

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THIS peculiar color variety was first called to my attention by D. C. Bell, M.D., of Ojai, California, who described it as "what ought to be a Palomino but isn't." His hesitation in classifying it with a true Palomino turns out to be due to the fact that it bears a different allele of the *A* (bay) gene, viz a^t, which characterizes the brown genotype.

He sent me a color photo of three colts, all sired by the same bay Morgan horse by claybank mares. One of them was a typical brown with a light muzzle and black mane and tail, genotype a^t-*B*-. The other two were much lighter in color, uniform reddish yellow, but with mane and tail of a slightly darker shade. Dr. Bell describes them as claybanks, the genotype of which I believe to be a^t-*bbD*-, as already stated.

This interpretation of the genotype of the claybank was strongly supported by data supplied by Mr. Louis Guilliams of Fort Collins, Colorado, based on a puzzling color variety which he had observed in the stud of his father's Quarter horses.

He described this as "red dun" and supplied a color photo of an example, Handy Scoot P-82-405, whose sire, Handy Britches P-38-228, was also described as red dun, the dam being Scoochi P-42-083, described as light sorrel.

He added, "as a matter of interest," that Handy Britches when mated to a Palomino mare sired a pseudo-albino colt. This would show him to have been a carrier of gene *D*, as was also his Palomino mate, and the pseudo-albino colt would accordingly be a cremello (*bbDD*).

The color photo of Handy Scoot is very similar to the pictures of the claybank colts supplied by Dr. Bell, and to a color photo of Handy Britches. In both the general body color is reddish

(Continued on page 128)

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THE SPRINGVILLE MOUSE

Further Observations on a New "Luxoid" Mouse

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A NEW "luxoid" condition in mice has been reported previously[5]. The description of the lesion has been presented together with some observations on its transmission and possible relationship with polydactylia. Luxoid has many characteristics in common with the other luxoid and luxate conditions reported by Rabaud[4], Carter[1] and Green[3]. However, the new luxoid differs significantly from these older reported hemimelic conditions.

In order to analyze the new luxoid embryologically and genetically and to test for genetic identity with the other luxoids, the new luxoid has been given to Dr. Forsthoefel of the University of Detroit, who has had experience in this field with other luxoid conditions[2].

It is clear that the new condition is a complex syndrome, consisting not only of the morphological characters listed previously, but also of many other manifestations[5]. It becomes necessary, therefore, to attempt to analyze this hemimelic syndrome and to place it upon a genetic basis if possible. It is proposed to identify the first gene responsible for some of this luxoid syndrome (if not all) as *ls* (luxoid-Strong or Strong's luxoid).

It is the purpose of this paper to record some of the observations on the appearance of this syndrome in direct lineal descent without an outcross from the mouse that showed the original luxoid condition. Dr. Forsthoefel's work will be based primarily upon an outcross to mice of the C57 strain and his analysis, therefore, of the character or characters will be made on a C57 background. His first paper (now in preparation) will, however, include his observations on the morphology and genetics of Strong's luxoid in the strain of origin. A few comments on the probable genetic nature of the syndrome will be presented here, but only provisionally.

Results

The penetrance of polydactylia in the descent that gave rise to the new luxoid syndrome has increased from 2.5 percent in the F_1 to about 93 percent in the F_{26} generation of inbreeding. Some female mice have produced 100 percent penetrance of polydactylia in their offspring without the appearance of luxoid, and recently a pair of luxoid mice have shown luxoid in their offspring without the presence of polydactylia. This situation may be brought about by a new mutation of the original gene to a form which causes hemimelia without polydactylia. However, the final analysis of "crossing-over" or new mutation or some other explanation cannot be determined by the present data. These observations differ significantly from those by other investigators where the data seem to indicate that the older luxoids are the ultimate homozygote of polydactylia. However, more data are required on the new luxoid before a final genetic analysis may be made. In one of the collateral descents of polydactylia there has been a change in that the degree of morphological expression of polydactylia has been greatly affected (about 100 percent penetrance) without the appearance of luxoid. The affected hind feet are about two to three times normal size but this increase is largely confined to the hallux. Finally there has also been a change of penetrance of polydactylia in the reverse direction. From an origin of a line of descent giving 92 percent penetrance of polydactylia, female 46801 produced progeny that showed only 11.0 percent penetrance of polydactylia in their progeny (1517 normal toed to 188 polydactylous). Female 46801 gave only one polydactylic offspring in her immediate offspring in contrast to 75 normals (penetrance of polydactylia of 1.3 percent). Forsthoefel by private communication reports that he has good evidence "that my subline of your strain in which Strong's luxoid gene originated carries at least one gene for polydactyly with low penetrance, besides the Strong's luxoid gene which on my hypothesis causes polydactyly in heterozygous condition very frequently. The former polydactyly is not nearly as great as the latter, but probably acts to intensify

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the expression of the latter when both are present together. Perhaps the different lines showing varying expressions and especially penetrance of polydactyly involve segregation and fixation of various numbers of genes making for polydactyly in the original source."

The data obtained in the lineal descent of the original mouse which produced the new luxoid are presented in Table I. The five series given in this report cover the generations of inbreeding in direct lineal descent between F_5 and F_{28}. The series of Strong and Hardy published in 1956[5] are repeated in this table in order to keep the data of common descent in one place (series 1). To this original subline four others (series 2-5) have been added from time to time.

The complete luxoid syndrome including anemia has always been lethal, the young all dying within 24 hours after birth. However, if the syndrome is not complete, especially if anemia is not present, many of these so-called "special luxoids" are viable. Many special luxoids reach sexual maturity and reproduce not as readily as the normal controls either with or without polydactylia but sufficiently to keep a continued descent of special luxoid by special luxoid for several generations.

The percentage of normal mice in the five series has not changed significantly. The percentages of normals in the five successive series were 27.06, 26.12, 28.89, 26.55 and 25.31. In the F_{21} generation of inbreeding four brothers were outcrossed to female mice of the C57 inbred stock. One male had polydactylia on both hind feet; one on the right hind foot only; one on the left hind foot only; and one showed no polydactylia whatever. The penetrance of polydactylia in the F_1 is given in Table II. Since the "normal" male showed the same penetrance of polydactylia in the F_1 as his brothers having the condition on either the left, or both hind feet, it must have been a somatic overlap. What percentage of somatic overlaps occurred in the so-called normal segregating population was not determined.

The percentage of mice with some hemimelic* manifestations also has not changed. These values were 72.94, 73.88, 71.11, 73.45 and 74.69. There appears to be a drop in the percentage of mice showing polydactylia on either one or both hind feet. These percentages are in sequence 59.08, 56.73, 36.73, 47.39 and 24.74. The penetrance of polydactylia on three feet has been in the five successive series 1.91, 2.99, 19.51, 7.75 and 11.12. Forsthoefel reports that in his experience "with Strong's luxoid gene, all manifestations of polydactyly only, whether on one or both hind feet, or including one or both forefeet, have bred as being only carriers of the gene. Polydactyly appears on the forefeet as a stronger expression of the carrier condition."

It is a very interesting fact that if polydactylia occurs on only one hind foot the right one is affected more frequently than the left; however, if a mouse has polydactylia on three feet, both hind feet are affected but the left front is involved more frequently than the right front.

TABLE I. Five series covering the generations of inbreeding in direct lineal descent between F_5 and F_{28}

Series	Total mice	Normal	% Normal	Hemimelics	% Hemimelics	Poly Hind Feet	% Poly Hind Feet	Poly 3 Feet	% Poly 3 Feet	Poly 4 Feet
1	1777	481	27.1	1296	72.9	1040	58.5	34	1.9	8
2	601	157	26.1	444	73.9	341	56.7	18	3.0	1
3	661	191	28.9	470	71.1	243	36.8	129	19.5	30
4	2606	692	26.5	1914	73.5	1235	47.4	202	7.8	16
5	1762	446	25.3	1316	74.7	436	24.6	196	11.1	134
Total	7407	1967	26.6	5440	73.4	3295	44.4	579	7.8	189

Series	Total mice	% Poly 4 Feet	Complete Luxoid	% Complete Luxoid	Special Luxoid	% Special Luxoid	Total Luxoid	% Total Luxoid
1	1777	0.5	201	11.3	13	0.7	214	12.0
2	601	0.2	81	13.5	3	0.5	84	14.0
3	661	4.5	40	6.1	28	4.2	68	10.3
4	2606	0.6	363	13.9	98	3.8	461	17.7
5	1762	7.6	248	14.1	302	17.1	550	31.2
Total	7407	2.6	933	12.6	444	6.0	1377	18.6

*Hemimelic and hemimelia are used in this paper in the sense defined in Dorland's *The American Illustrated Medical Dictionary*, "A fetus with defective limbs."

Penetrance of polydactylia on all four feet without any evidence of luxoid has been in successive series 4.5, 0.16, 4.53, 6.13 and 7.60 percent.

During the time of the present experiment the penetrance for the complete luxoid syndrome has not changed, being 12.6, 13.4 and 6.0 percent in the first three series and 14.0 and 14.1 percent in the fourth and fifth series. An inspection of Table I will disclose that the new luxoid is increasing in penetrance from 12.0, 13.9 and 10.2 percent in the first three series to 31.2 percent in the fifth series. However, this increase is due mostly to the increase of the special luxoid class where the degree of manifestation of the character is not as complete as in the luxoid class. There has been an increase of the special luxoids from 0.7, 0.5 and 4.2 percent penetrance in the first three series to 17.1 percent in the fifth series.

Thus the analysis of the data in Table I shows that the most significant change in penetrance of any characteristic in the successive series has been in an increase of mice showing the partial or incomplete luxoid syndrome (referred to as special luxoids), concomitantly with the loss of the class showing polydactylia alone on the hind feet. These observations can be explained on the basis that the hemimelic condition is increasing in severity in the successive series through the process of inbreeding. This could be due to the loss of modifying factors through inbreeding.

There appears to be a very strong correlation between the luxoid character and polydactylia. However, the evidence already obtained indicates that this correlation can be broken. Thus the conclusion that the luxoid syndrome is the ultimate homozygote of polydactylia apparently does not apply here. A concept of close linkage may be indicated. Another mutation at the *ls* locus may also be involved. This genetic situation may eventually be resolved.

The fact that somatic overlaps may exist in a segregating population may interfere with a final genetic analysis without genetically testing out each individual against a standard inbred strain, such as the C57.

Several sublines for the appearance of radically different degrees of polydactylia have occurred suddenly even after 20 generations of inbreeding. This would indicate that there is a certain degree of genetic instability associated with the manifestation of these biological characteristics. One concept would be that a single gene is unstable. However, it will take further testing to demonstrate that other loci may be involved in this genetically unstable state.

It is possible that cytological examinations on this particular polydactylous descent may disclose some chromosomal aberrations responsible for this observed unstable biological situation rather than an unstable gene.

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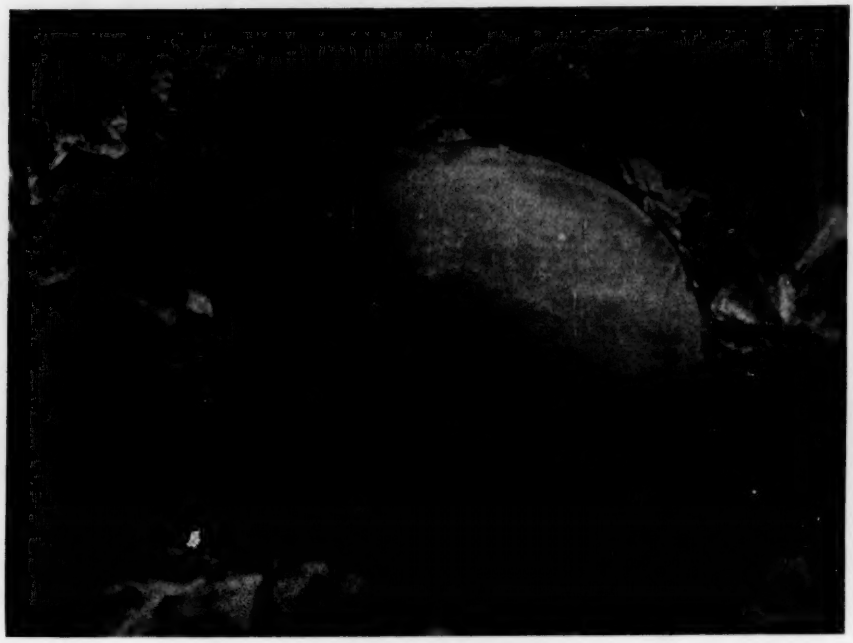
TABLE II. Penetrance of polydactylia in the F_1

Father showing polydactylia	Polydactylia				Percent Polydactylia
	Both	Right	Left	None	
Both	1	13	5	108	14.96
Right	1	4	5	110	8.33
Left	0	12	13	132	15.92
None	2	10	12	134	15.19

SHIPPER, A NEW FUSARIUM WILT-RESISTANT WATERMELON

S. S. IVANOFF*



SHIPPER WATERMELON

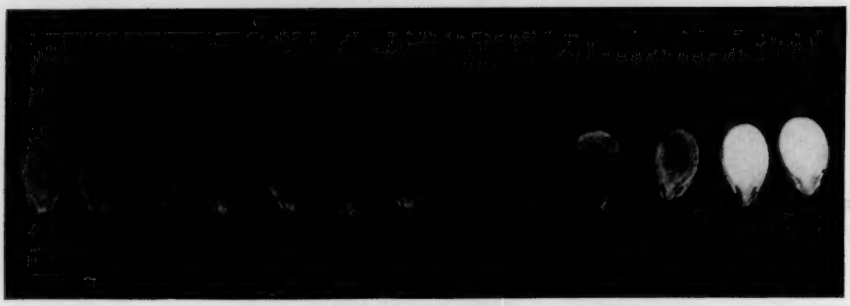
Figure 11

Shipper, the new wilt-resistant, dark green watermelon shortly before harvest.

FOR some time a need has been felt by watermelon growers and shippers for a dark green, round-type melon to take the place of older varieties of this type which lack certain desirable traits, namely, good shipping and high internal qualities combined with high resistance to Fusarium wilt. The wilt-inducing fungus, *Fusarium oxysporum* f. *niveum* (E. F. Sm. Snyder & Hansen), is a persistent soil inhabitant, and no practical fungicidal control is available.

Recently new disease-resistant melons have been produced by plant breeders, but no single type can satisfy all the needs of the industry, and some have been found wanting in quality. Other melons of very high quality possess only partial resistance to, or tolerance of, Fusarium wilt. In such varieties the incidence of death by wilting is less frequent than in susceptible kinds but they, nevertheless, show the effects of the wilt by reduced vine vigor, fruit size and yield.

*Department of Plant Pathology and Physiology, Mississippi State University, Mississippi Agricultural Experiment Station, State College, Mississippi. Journal Paper (New Series) No 909.



SEEDS OF SHIPPER

Figure 12

Seeds of the new watermelon vary from cream to brown, mostly brown of various shades. This is a distinguishing characteristic of the variety, helpful in seed certification, since the color of the other varieties of Black Diamond type is black.

Round or nearly round melons are preferred by the industry because they present lesser problems in loading and shipping than the elongated types. The traditional dark green color has a special appeal to some consumers.

Materials and Methods

Materials and methods were chosen with the aim to breed the highest possible wilt resistance into the new variety. An attempt was made, therefore, to incorporate within a single plant entity all the available genes for this kind of resistance, to be brought together from diverse origins and sources, so that the new variety could be grown quite safely and profitably on wilt-infested land. It is generally understood, however, that disease resistance alone, no matter of how high an order, is not sufficient to recommend a new variety to the trade. "Internal quality," a common commercial term employed to express a combination of various very desirable traits of the fruit, such as the color and compactness of the flesh, and freedom from excessive fiber, "white heart," "hollow heart," etc., is a most essential consideration in any breeding program. The ability to keep, haul, or ship is a characteristic determined by a combination of elemental traits of the rind, of the flesh, and of certain specific ripening processes within the fruit. And finally, such epicurean considerations as sweet tenderness and fine flavor are of ultimate importance to the consumer, and constitute a distinctive mark of this unique fruit.

Shipper was derived from four selected ancestors, all well known for their good eating qualities: the old Dixie Queen, which is round and wilt susceptible; and Klondike R7, Leesburg, and Blacklee, which are wilt resistant. (Klondike R7 was introduced by Dr. D. R. Porter of the University of California, while Leesburg and Blacklee were developed by Dr. N. M. Walker of the University of Florida.)

First, a cross was made between Dixie Queen and Klondike R7, the latter parent tracing its genes for resistance to the citron. An early F_4 inbred was then selected from this cross which had the round, striped appearance of Dixie Queen, but had also inherited the wilt resistance of Klondike R7. This important, round, shipping type of distinct flavor was sought as one of the three direct parents of Shipper, which were now all wilt resistant.

Next, the F_4 selection was crossed with Leesburg, a long, light green melon which originated as a natural wilt-resistant segregant (or perhaps as a mutant) in a large population of Klekley Sweet. This first-generation hybrid was then crossed with Blacklee, another long but very dark green and somewhat late

melon with a very tough rind, which inherited genes for wilt resistance from Leesburg, and from the Australian variety Hawkesbury. Seed of this triple cross was then planted in isolation in soil intensely infested with the wilt organism, and the best quality fruits from the most vigorous vines were saved.

During the next seven generations the chief task was to inbreed and select for type and quality.

"Toughness" of the rind, a prime shipping quality, was tested during the selective period by a very simple but reliable method. It takes into consideration the two individual components of "toughness" in tissues, namely, hardness and resiliency. Each component was found by this writer to be inherited independently and in a dominant manner[1].

The very high wilt resistance of Shipper was finally confirmed in comparative tests by artificial inoculations, and also by plantings on naturally wilt-infested soils in Mississippi, Texas, and Iowa.

Description

The following are the major characteristics of Shipper:

Shape: Near round like Black Diamond (Syn. Cannonball or Florida Giant), Figure 11.

Size: Will produce 30 to 35 pound shippers. On wilt-free soils the fruit is generally larger than Blackstone and somewhat smaller than Black Diamond. On wilt-infested soil, either partially or totally infested, it outgrows all other varieties of this type.

Rind: Dark green, relatively smooth, about ½ inch thick, tough (very hard but flexible); no weak points.

Flesh: Deep red; solid and very firm, which adds to its keeping and shipping qualities. "White heart" and "hollow heart" rare.

Seeds: Vary from cream to brown, a distinguishing varietal characteristic, Figure 12. (Other Black Diamond type melons have black seeds.)

Uniformity: Very uniform.

Disease Resistance: The wilt resistance of Shipper is very high and this characteristic is one of its best recommending features. Consequently, it may be grown quite successfully on Fusarium-infested soils. A comparison for yield on infested soils with the susceptible Black Diamond and with two other varieties of the same type possesing varying degrees of wilt resistance is shown in Table I.

Shipper is not resistant to anthracnose, and like all other commercial varieties is not resistant to gummy stem blight, an important cucurbit disease caused by the fungus *Mycosphaerella melonis* (Pass.)

TABLE I. Tests on wilt-infested soils with Shipper and three other watermelon varieties of the round, dark green (Black Diamond) type at two locations in 1957. (Data by H. C. Hudson and L. E. Peterson, of Texas and Iowa Agricultural Experiment Stations, respectively.)

		Nacogdoches, Tex.		Fruitland, Ia.
Variety	Disease resistance	Survival %	Yield lb/A	Yield tons/A
Shipper	Wilt resistant	93	10,839	8.0
Summit	Wilt resistant	----	----------	6.6
Blackstone	Partial resistance to wilt (good resistance to anthracnose)	60	3,952*	----
Black Diamond (check)	Very susceptible	0	0†	0.5

*Not marketable because of small size.

†Very small fruits on a few dead vines not included.

TABLE II. Tests on wilt-free soils with Shipper and other widely grown watermelon varieties in 1956-1957

	Crystal Springs, Miss.,* 1957		State College, Miss, 1956			
Variety	lb/A	Av. melon wt. (lbs.)	lb/A	Av. melon wt. (lbs.)	Av. total solids %	Flesh qualities
Shipper	18,942	24.1	22,419	26.8	11.6	very good
Blackstone	12,642	21.5	18,463	23.2	10.7	very good
Black Diamond	18,802	24.4	19,342	27.9	9.1	fair to poor
Congo	11,368	22.3	----------	-----	-----	----------
Charleston Gray	14,504	21.6	----------	-----	-----	----------

*The trial at Crystal Springs, Miss., was conducted by Dr. Steve Windham of the Mississippi Truck Crops Branch Experiment Station.

Chiu & J. C. Walker, to which no source of genetic resistance is now known.

Eating Qualities: Very good, sweet and tender. Percent total solids varies ordinarily from 9.0 to 13.0, and sometimes is higher.

Earliness: As early as Black Diamond and Charleston Gray (a popular long-type melon), sometimes earlier.

Yield: In the class of other prolific varieties (Table II).

Adaptability: Quite general. This variety will show its best advantage, however, in locations where the new land has already been used up, and growers are compelled to grow the crop on fungus-infested land where melons have been planted before, and where the pathogen may persist for many years.

(Shipper, prior to its naming and release, was experimentally tested by various investigators, seedsmen, and commercial growers under the designation "Mississippi 1717.")

Summary

A new watermelon variety named Shipper, highly resistant to Fusarium wilt, caused by *Fusarium oxysporum* f. *niveum*, and with high internal qualities and ability to ship, is described. It was derived in a breeding program from Dixie Queen, Klondike R7, Leesburg and Blacklee varieties. The fruit is medium to large, dark green, nearly round, with very tough rind (hard and flexible), compact but tender red flesh of high quality, and is early and uniform. The seeds are cream to brown, a distinguishing varietal characteristic. The variety has been tested with success in many locations in the United States but may be found particularly useful on old watermelon grounds long infested with the Fusarium wilt fungus.

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◆

Genetics of the Claybank Dun Horse

(*Continued from page 121*)

yellow, with mane, tail and legs of a slightly darker shade, but definitely not black.

The darker extremities in the claybanks, as compared with a Palomino, which has *lighter* extremities, would seem to be due to their having an a^t allele instead of A.

This interpretation is supported by data from a third independent source supplied by Dr. W. Ralph Singleton, Director of Blandy Experimental Farm, Boyce, Virginia.

A color photo made by him shows a brown mare with her two colts by the same sire, a registered Quarter Horse stallion, Poco Buck. One of the colts, Pegasus, is a two-year-old cremello with a light brown (not white) mane and tail, genotype a^t-$bbDD$. The other colt is a typical brown, a^t-BB or a^t-Bb, like the dam. The chances are even that she may also be a carrier of D, as were both her mother and father.

A color photo of a claybank was supplied from a fourth independent source, by Professor W. G. Steele of Lexington, Kentucky. This agrees with the pictures supplied by Dr. Bell and Mr. Guilliams in showing a horse with a general yellowish body color, a lighter yellow muzzle and darker mane and tail.

Odriozola[2] lists as a distinct color variety claybank dun of of the United States. He gives its genotype (in equivalents of our nomenclature) as $bbDd$. This I regard as correct as far as it goes. It would put the claybank in the same general category as the Palomino but makes no suggestion as to what allele of gene A it carries. This is a vital matter in discriminating a claybank from a Palomino, as is indicated by Dr. Bell's independent observations.

All the available evidence agrees in indicating for the claybank a genotype of a^t-bbE-(or ee)Dd-, whereas the Palomino is definitely known to be of genotype A-bbE-(or ee)Dd-.

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A PEDIGREE ANALYSIS OF ABERDEEN-ANGUS CATTLE

J. I. Sprague, Jr., W. T. Magee and R. H. Nelson*

THE increased frequency of dwarfism in beef cattle during the past 10 to 15 years has stimulated interest in pedigrees and the relative importance of certain strains and individual bulls in the various breeds. In the hope of shedding some light on the dwarfism situation, pedigrees of Angus cattle were analyzed using the method developed by Wright and McPhee[5].

The objectives of the study were: (1) to determine the *inter-se* relationship and the amount of inbreeding occurring during the past 20 years, (2) to determine the more important bulls in the breed — particularly during the past 15 to 20 years, and (3) to determine the relative importance of these cattle.

Stonaker[3] reported the amount of inbreeding and *inter-se* relationship in five samples of the Angus breed born in the United States in 1900, 1910, 1920, 1930 and 1939. The amount of inbreeding expected on the basis of the breed's over-all *inter-se* relationship was 62 percent of that actually found. There was a tendency for mates to be more closely related than if mating had been done absolutely at random throughout the breed. The more important sires of the breed were found to be Black Prince of Tillyfour, Hanton, Young Viscount, Rob Roy McGregor, Grey Breasted Jock and Pat. More recent sires of importance were Earl Marshall and his son Blackcap Revolution.

The method of Wright and McPhee has been used in analyzing the breeding structure of several breeds of cattle as well as several breeds of other species. Willham[4] and Carter[1] reviewed the studies made previous to 1940. Work not discussed in these papers includes the study of Brown Swiss cattle in the United States by Yoder and Lush[6], and the Arabian horse by Zaher[7].

Procedure

Four samples of pedigrees from the Angus breed, each sample consisting of 400 pedigrees (200 animals of each sex), were studied. The samples were drawn from cattle born in 1940, 1945, 1950 and 1955. They were sampled from the American Aberdeen-Angus Herd Book. A random line from the sire and another from the dam of each pedigree were traced to the earliest animal for which dates were recorded.

The percent inbreeding and the percent *inter-se* relationship were calculated for the breed at each of the four periods.

These pedigrees were then analyzed for important common ancestors by a count of the number of times the ancestors appeared in the study. The relative importance of these ancestors was determined by calculation of direct, collateral and total relationship of these animals to the breed, according to the method of Stonaker[2]. In assessing the values for collateral relationship, the six closest relatives of the ancestors were used, i.e., sire, dam and both grandsires and grandams.

Results and Discussion

Inbreeding and inter-se relationship

The inbreeding and the *inter-se* relationship percentages for the years 1940 to 1955 are reported in Table I. Stonaker's earlier results are also reported for the reader's convenience.

The inbreeding has not shown any particular trend since 1940, and it would appear the inbreeding has remained at about the same level since 1910 with exception of small short-time variations. For the most part these were within

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one standard deviation of the over-all mean.

The *inter-se* relationship has been declining continuously since 1940. Stonaker's results show that except for 1920, this value has declined steadily since 1910. A decline would be expected because of the rather rapid breed expansion during this period. Evidence of this expansion in purebred Angus cattle is reported by the American Angus Association. Their report shows that the registrations of Angus cattle have increased 736 percent from 1940 to 1959.

Expected inbreeding

The expected inbreeding with random mating throughout the breed (see Table I) was calculated by the formula R/2-R, R representing the *inter-se* relationship. This value showed a continuous decline since 1930. The inbreeding expected was 44 percent of that actually found for the 1940 to 1955 span, while an average of 62 percent was reported by Stonaker for the 1900 to 1939 period. This drop in expected inbreeding as a percent of that observed is an indication of family development. The more likely causes for the difference between actual and expected inbreeding are possibly: (1) limited exchange of breeding stock between geographic areas of the United States and (2) linebreeding tendencies on the part of some breeders.

Short term fluctuations

Short term fluctuations of the inbreeding in the present study are shown graphically in Figure 13. Stonaker reported the lowest inbreeding values in his analysis when the numbers sold at auction were the highest. This same trend was noted in the 1955 analysis. In that year the inbreeding was the lowest of the four periods studied and the number of Angus cattle sold at auction was the highest. This finding would tend to support Stonaker's hypothesis that the economy of breeding purebred cattle affects the percent inbreeding. However, because of the small amount of variation in the inbreeding from 1940 to 1955, the short term fluctuations in inbreeding in the present study were considered inconclusive.

TABLE I. Inbreeding and *inter-se* relationship in Aberdeen-Angus cattle

Year	Inbreeding	*Inter-se* relationship	Expected inbreeding
1900*	8.9±1.8	9.4	4.9
1910*	12.7±2.2	16.3	8.8
1920*	10.8±2.0	12.3	6.5
1930*	14.2±2.4	16.1	8.8
1939*	11.3±2.2	13.3	7.1
1940	13.2±2.1	12.0	6.4
1945	12.9±2.1	10.8	5.7
1950	14.5±2.1	11.0	5.8
1955	12.3±2.1	10.0	5.3

*From Stonaker[3].

SALES AND INBREEDING
Figure 13

Comparison of sales at auction and inbreeding during the years 1940-1959.

Important animals

Total relationship is a measure of the genetic association of an individual to the breed as a whole. Table II lists the important individuals found in this study. The bulls are listed in decreasing order of their total relationship as calculated for 1955. There are three groups of bulls in the Angus breed which give total relationships to the breed in a far greater amount than their contemporaries. The most important bull was Earl Marshall 183780, born in 1913, and his son Blackcap Revolution 287269, born in 1919. There are two other groups of bulls which give total relationship of relatively high magnitude. One is the Eileenmere strain which traces back to Black Woodlawn 42088 (born 1900), and his son Oakville Quiet Lad 109220 (born 1906), who in turn was the sire of Eileenmere 4th 251504 (born 1917). It was noted that a half-brother-sister mating produced three of the foundation Eileenmere animals. Eileenmere 4th, 32nd and 487th were double grandsons of Black Woodlawn, Eileenmere 4th and Eileenmere 32nd, respectively. The third important group is Earl Eric of Ballindalloch 100422 (born 1904) and his son Elgon 111375 (born 1907). All of the bulls were born in the 1900 to 1920 period. These three groups have shown remarkably steady total relationship in all four of the current periods.

Using 1955 as a base year, there are several bulls born since 1930 which have total relationship percentages greater than other bulls born in the same period. Among these are Eileenmere 85th 470007 (born 1933), Eileenmere 487th 668743 (born 1940) and Black Prince of Sunbeam 504521 (born 1935). All of these bulls have gained considerably in their relationship since 1940.

Expected appearance in a random pedigree

How many times would a bull be expected to appear in a pedigree picked at random and traced back to the generation of the birth of the bull? To answer this question the authors proposed the following method of calculation. If the direct relationship to the breed and the birth date of a particular ancestor are known, then the number of expected appearances of that ancestor in an average pedigree can be determined from the following formula:

$x = R_i\, 2^m$, where

x = the expected number of times in an average pedigree the ancestor would appear,

R_i = direct relationship of the ancestor to the breed in year i,

$$m = \frac{(\text{year i} - (\text{ancestor's birth date} + 2\text{years}))}{5.4},$$

or the number of generations from the time the first offspring was born to year i.

The distribution of this expected number has not been determined but it appears to approximate the binomial distribution for animals which have a direct relationship to the breed of .01 or larger. Thus the variance of x is calculated directly from the variance of the binomial. The n needed for calculating the variance of x, using the binomial distribution, is $2^m/4$. The number of animals in a pedigree m generation back from year i is 2^m. The reason for dividing 2^m by 4 to obtain n is it has been noted that most animals have four different grandparents; thus if an ancestor appeared as one of the grandparents, his chance of appearing again in that four is small. The sets of four are the sets of grandparents of the animals born two generations after the time of the animal in question. For example, in the tenth generation of a pedigree there are 1024 animals, but only 256 groups of grandparents of the animals of the eighth generation. Therefore, there are only 256 independent places an animal could occur in the tenth generation of a pedigree. Or stated another way, half-sib matings do not often occur. To the extent the breed is divided into family groups, this estimate of the variance gives too small an estimate of the true variance in the population.

The expected times Earl Marshall would appear in an average pedigree of animals born in 1955 would be calculated in the following manner:

$x = R_{1955} 2^m$; therefore,

$x = (.115)\ (2^{7.4})$

$x = 19.5$

$V(x) = 10.5$

A list of important bulls and their expected number of appearances is included in Table III.

Summary

The inbreeding of the Angus breed remained about constant and the *inter-se* relationship declined slightly as measured in four samples taken from the cattle born in the years 1940, 1945, 1950 and 1955.

The inbreeding expected based on the *inter-se* relationship was 44 percent of the actual calculated inbreeding for this 15-year period.

Evidence was presented to support the hypothesis proposed by Stonaker, that inbreeding was affected by economic trends as measured by the number of animals sold at auction. However, the variation in amount of inbreeding was so small that short-time trends in inbreeding were inconclusive.

The important bulls born between 1900 and 1920 were discussed. The first important

TABLE II. Important ancestors of the Aberdeen-Angus breed

Ancestor	Relationship to the breed							
	1955		1950		1945		1940	
	Direct	Total	Direct	Total	Direct	Total	Direct	Total
Earl Marshall 183780 Born 1913	11.5	12.4	9.4	10.4	9.9	10.7	10.4	11.0
Blackcap Rev. 287269 Born 1919	6.1	11.0	7.7	10.7	6.3	13.4	5.1	9.3
Black Woodlawn 42088 Born 1900	7.6	8.7	4.2	6.2	9.2	10.6	7.9	8.6
Oakville Quiet Lad 109220 Born 1906	4.4	7.9	2.9	5.5	3.7	7.9	4.7	8.1
Eileenmere 85th 470007 Born 1933	4.5	7.3	3.3	4.8	1.9	3.4	0.3	1.4
Eileenmere 4th 251504 Born 1917	2.9	6.1	3.4	6.8	2.1	5.0	1.6	4.9
Eileenmere 15th 398457 Born 1924	3.6	5.5	3.6	5.0	3.1	4.9	2.5	3.6
Eileenmere 487th 668743 Born 1940	2.9	5.5	0.9	2.9				
Earl Eric of Ballindalloch 100422 Born 1904	3.5	5.4	4.4	6.8	5.2	6.5	4.2	5.7
Eileenmere 32nd 428072 Born 1928	4.8	5.4	3.6	4.3	2.9	3.8	4.8	5.1
Elgon 111375 Born 1907	2.2	5.0	1.5	3.0	1.4	4.2	1.0	3.1
Blackbird Bandolier of Page 414214 Born 1927	2.1	4.0	0.6	3.1				
Black Prince of Sunbeam 504521 Born 1935	2.8	3.4	1.5	1.8				
Black Bardolier 480883 Born 1934	1.2	2.1	0.4	0.9				

group was the bull Earl Marshall and his son Blackcap Revolution. The second group was the bull Black Woodlawn and his son Oakville Quiet Lad and his grandson Eileenmere 4th. The third group was the bull Earl Eric of Ballindalloch and his son Elgon.

The bulls born since 1930 with high total relationship to the breed were Eileenmere 85th, Eileenmere 487th and Black Prince of Sunbeam.

A method of calculating the expected number of appearances of an ancestor in a pedigree was proposed.

TABLE III. Expected appearances (X) in a random pedigree

	X	S.D.
Earl Marshall 183780	19.4	3.2
Blackcap Revolution 287269	4.5	1.8
Black Woodlawn 42088	67.7	6.1
Oakville Quiet Lad 109220	15.9	3.6
Eileenmere 85th 470007	0.6	0.7
Eileenmere 4th 251504	3.0	1.6
Eileenmere 15th 389457	1.5	1.1
Eileenmere 487th 668743	0.6	0.7
Earl Eric of Ballindalloch 100422	19.2	4.0
Eileenmere 32nd 428072	1.1	0.9
Elgon 111375	8.0	2.7
Blackbird Bandolier of Page 414214	0.6	0.7
Black Prince of Sunbeam 504521	0.3	0.5
Black Bardolier 480883	0.1	0.3

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